

SEQUENCE LISTING

<110> Wilting, Reinhard
Ostergaard, Peter
Lassen, Soren

<120> POLYPEPTIDES OF ALICYCLOBACILLUS SP.

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<170> PatentIn version 3.2

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gcgatggggc tgcagacgga cggcattgtg ggtcccctga cctggggggc tttggcgaag	360
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caagtcgaat ggaagcgcat cgtatggaac ggaggttga tttcgaagcc catcggcttc	480
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tccaacgtca ccggcaactc gacgggcaac agtttgggga actcgacggg caacagcttg	1020
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ccgtccaaca tcaatgcgca gagcatcaac cagtttctgc tgcagaacag ctcgccgctc	1200
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<210> 10
 <211> 1791
 <212> DNA
 <213> Alicyclobacillus sp.

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 <222> (1)..(1791)
 <223> CDS

<220>
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 <222> (1)..(147)
 <223> sig_peptide

<220>

<221> misc_feature

<222> (148)..(1791)

<223> mat_peptide

<400> 10

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gccctgcaag	ccatgacgtt	caacggcacc	gcgccagggc	cgttgcttgt	ggcccatcaa	360
ggcgacgtcg	tgaaggtcac	ggtgcacaac	cgctctccg	tccctctgac	cattcactgg	420
cacggcatcg	cggtgcccgg	cgcggaagac	ggcgctccctg	gtgtcacgca	aaacccaatt	480
ccgcctggcg	ggagctacac	gtacgagttt	cagggttaacc	agcccggaac	gtactggtac	540
cactcgcacg	aggcgagctt	tgaagaggtg	ggcctcgggt	tgtacggcgc	cttcgtcggt	600
ctgccc aaac	gggcggtcca	tccggccgat	cgcgactaca	cgctcgtcct	gcacgagtgg	660
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gacgcctggt	cacaattcaa	ggagacggat	gcagcgagcc	ttgaacgagc	gccgtgggtc	1320
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<210> 11
 <211> 735
 <212> DNA
 <213> Alicyclobacillus sp.

<220>
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 <222> (1)..(735)
 <223> CDS

<220>
 <221> misc_feature
 <222> (1)..(87)
 <223> sig_peptide

<220>
 <221> misc_feature
 <222> (88)..(735)
 <223> mat_peptide

<400> 11	
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aacgcgccgg acacgtgtc caatgaaacc ggccagacgc tcgatacggc caaccgccg	180
tacctgcaca cgtcgaccga gcagtggaag agcatgccga agatgttcat caaccgaac	240
aagacctatg acgccattgt ccacaccaat tacgggacgt tcaccatcca gctgttcgcc	300
aaagacgcgc ccatcacggt gaacaacttc gtgttcctgg cagagcaciaa cttctaccac	360
gattgcacgt tcttccgcat cgtgaagaac ttcgtgattc aaacgggcga tcctcgcaac	420
gacggtaccg gcggcccggg ctacaccatc ccagatgaac tcagccatca ggtgccattc	480
acgaagggca ttgtcgcgat ggccaacacg ggccagccgc acacgggcgg aagccagttt	540
ttcatctgca cggccaatga cacgcaggtc ttccagccgc ccaacaatcg ctatacggaa	600
ttcggccgcg tgatctccgg aatggacgtg atcgacaaga ttgccgcat cccggtgacc	660
gaaaacccca tgacgcagga agacagctat cctctgaaga ctgcgtacat cgagtcgatt	720
caaattcaag aatcg	735

<210> 12
 <211> 1824
 <212> DNA
 <213> Alicyclobacillus sp.

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 <222> (1)..(1824)
 <223> CDS

<220>
 <221> misc_feature
 <222> (1)..(81)
 <223> sig_peptide

<220>
 <221> misc_feature
 <222> (82)..(1824)
 <223> mat_peptide

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 attcatcacc tcgtcgtcat ctccgacgag aacgtctcct ttgatcacta tttcgccacc 180
 tatccgaacg ccgccaatcc agccggcgag ccgccctttt acgccgcgcc gggcaccctg 240
 agcgtcaatg gcctgtccgg aagccttctc acgcacaatc ccaacggcgt gaatccgcag 300
 cgcctcgacc gttcccaagc cgtgacgccg gacatgaacc acaactacac gccggagcag 360
 caggccgtgg acggggggccg catggataac tttatcaata cggtcggccg cggaaatccc 420
 atcgatctcg actactacga cggaaacacg gtcaccgcgc tctggtatta cgcgcaacac 480
 ttcgccttga acgacaacgc gtactgcacg cagtacggcc cgtctacgcc tggcgccatc 540
 aacctgattt cgggcgacac cgcgggagcg acggtttatt cttcaagtga gaccagcggc 600
 gccgcacaag tcgtgccacc cggcagcaaa aactttccga atgccgtgac gccaaacggc 660
 gtcgacatcg gcgacatcga tccctactac gacagcgcct ccaaaggcat gaccatggcg 720
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 cagggcggtt ttgcaaatcc gaacgccaag gacaacaata tcgccggcac agatgaaacc 840
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 catctgccgc ctacgagcgt ggcgatgatc gggcgcacgg atcaggcaaa ccaccagtac 960
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gtgtccccag atatgcagcc ggaggtcatt cgcggcacca cgtatctcag cctgaatcac	1560
tacgctcaaa acctcgatgt cgtgctgcaa acctctcggg ggatggcgcg gttctcctac	1620
gaggggcacg aggtcgagat cgacgagcgt tccgggcttg tccgggtcga tggcgaagcg	1680
gtccatctca aggcgcctct tgtgcgggtg gacggcgtat ggatggtgcc cgtagaggaa	1740
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ctcttttctc cgcaagacgc ccat	1824

<210> 13
 <211> 750
 <212> DNA
 <213> Alicyclobacillus sp.

<220>
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 <223> CDS

<220>
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 <222> (1)..(75)
 <223> sig_peptide

<220>
 <221> misc_feature
 <222> (76)..(750)
 <223> mat_peptide

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caagcccaaa gggccattta caaggtggac acgaaggaaa aggtggctgc tctcacgttc	180

gacatctcat gggggcaccg cacgcccga cccgttctcg agacactcaa gaagtgcggc	240
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aagaaaatca aggcgatggg ctacgaaatt ggcagccatg ggtacctgca caaggactat	360
tccaattacc cggactcttg gattcgagaa caggcgatgc tcgcagacaa ggccattcaa	420
caggctactg ggggtcaagcc gaagctgttc aggacgcaa atggcgactt gaatccgcgc	480
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gactggaaaa acccaggcgt cgacgcgatc gtcaaccgcg tcacgaagcg cgtgggtgcct	600
ggcgatatca tcctgatgca cgcgagcgac tcgtccaaac agattgtgga ggccctgccg	660
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gcgggcgcca gcgttcaatc caaggtccag	750

<210> 14
 <211> 972
 <212> DNA
 <213> Alicyclobacillus sp.

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 <223> CDS

<220>
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 <222> (1)..(63)
 <223> sig_peptide

<220>
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 <222> (64)..(972)
 <223> mat_peptide

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tcggcacatg tgtgggaaga agtcagccgc acgtggggaa cgcttcccgt cgatgcccgc	180
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ccgccgaagc gaagactcgg agacctttcg cccgacgtga tttaccgcgg ccccgcgag	360
gagaagtcgg tggcgctgat ggtgaatgtg tcctggggcg atgcgtacgt gccaggatg	420

cttgaggtgc tgcgcagcgc gcacgtgaag gccacgtttt tcgtggacgg cgcgtttgcg	480
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gaggccctgc ctgatgtgat ccgctggctc gaggggcacg gttatcggct gaaaacggtg	900
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ttccacagcg cg	972

<210> 15
 <211> 642
 <212> DNA
 <213> Alicyclobacillus sp.

<220>
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 <222> (1)..(642)
 <223> CDS

<220>
 <221> misc_feature
 <222> (1)..(87)
 <223> sig_peptide

<220>
 <221> misc_feature
 <222> (88)..(642)
 <223> mat_peptide

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gagaacggtc agccggttcc ggccaaaatt ggccggcacga cgaacaacat tccggccgtc	360
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<210> 16
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 <212> DNA
 <213> Alicyclobacillus sp.

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 <223> CDS

<220>
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 <222> (1)..(63)
 <223> sig_peptide

<220>
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 <222> (64)..(771)
 <223> mat_peptide

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gttgcgcccg cggcgccagg cggctccgcc tcgatgcaaa accggcatat tctgcaggag	180
ccgctgccgc gtggcggtgaa aacggaaacg gatttgtaca actggctttt atggcagaga	240
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gcgtcgagat cgcgcagggc aaagtcgatg gcgcgctgcc aaaagtcagg ttgcgtgaga	660
tccgcaccga tgtgtttttt ggccagatcc tcgaccgcga tgcgaccggt gtcgcgaagc	720
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<210> 17
 <211> 3390
 <212> DNA
 <213> Alicyclobacillus sp.

<220>
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 <222> (1)..(3390)
 <223> CDS

<220>
 <221> misc_feature
 <222> (1)..(72)
 <223> sig_peptide

<220>
 <221> misc_feature
 <222> (73)..(3390)
 <223> mat_peptide

<400> 17
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<210> 18
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 <212> DNA
 <213> Alicyclobacillus sp.

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 <223> CDS

<220>
 <221> misc_feature
 <222> (1)..(123)
 <223> sig_peptide

<220>
 <221> misc_feature
 <222> (124)..(744)
 <223> mat_peptide

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acaacttctt	tggttaattc	gacgaatagt	tcacaggtag	caaagcaaga	gcaaaactcg	240
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ggagacttgg aaattagagt taactccctg cagcaagtta agagtgtggg gtacgacggg	420
ataggtgaaa ccgcaaattg tgcgttttgg gttatcaaca tcaccataag aaatgacgga	480
tccactccta tggagggtcgt tgatggcata ttccatttgc agaacttaaa cgggaacggt	540
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<210> 19
 <211> 516
 <212> DNA
 <213> Alicyclobacillus sp.

<220>
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 <222> (1)..(516)
 <223> CDS

<220>
 <221> misc_feature
 <222> (1)..(75)
 <223> sig_peptide

<220>
 <221> misc_feature
 <222> (76)..(516)
 <223> mat_peptide

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gccccggtgg caggcgcgac ggtgacggcc ggcggcacgc tgaaggtagag cggccaagtg	300
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ctcgtgcagc agatcgtcgg tacgaatagc accggcgcgt tcgtggacac gctcaagctt	420
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<210> 20
 <211> 726
 <212> DNA
 <213> Alicyclobacillus sp.

<220>
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 <222> (1)..(726)
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<220>
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<220>
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 <223> mat_peptide

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tattttctcc ttgagttttt ggcgaaatcca attgtcgcgg ccattgctgt gcccaccact	660
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tacagc	726

<210> 21
 <211> 540
 <212> DNA
 <213> Alicyclobacillus sp.

<220>

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 <222> (1)..(540)
 <223> CDS

<220>
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 <222> (1)..(72)
 <223> sig_peptide

<220>
 <221> misc_feature
 <222> (73)..(540)
 <223> mat_peptide

<400> 21
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<210> 22
 <211> 1431
 <212> DNA
 <213> Alicyclobacillus sp.

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 <223> CDS

<220>
 <221> misc_feature
 <222> (1)..(75)
 <223> sig_peptide

<220>
 <221> misc_feature
 <222> (76)..(1431)
 <223> mat_peptide

<400> 22
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<210> 23
 <211> 1020
 <212> DNA
 <213> Alicyclobacillus sp.

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<223> CDS

<220>

<221> misc_feature

<222> (1)..(57)

<223> sig_peptide

<220>

<221> misc_feature

<222> (58)..(1020)

<223> mat_peptide

<400> 23

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<210> 24

<211> 1023

<212> DNA

<213> Alicyclobacillus sp.

<220>

<221> misc_feature

<222> (1)..(1023)

<223> CDS

<220>

<221> misc_feature

<222> (1)..(87)

<223> sig_peptide

<220>

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<222> (88)..(1023)

<223> mat_peptide

<400> 24

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gcg	1023

<210> 25

<211> 1197

<212> DNA

<213> Alicyclobacillus sp.

<220>

<221> misc_feature
 <222> (1)..(1197)
 <223> CDS

<220>
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 <222> (1)..(84)
 <223> sig_peptide

<220>
 <221> misc_feature
 <222> (85)..(1197)
 <223> mat_peptide

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<210> 26

<211> 959
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(24)

<220>
 <221> mat_peptide
 <222> (25)..(959)
 <223> acid endoglucanase or acid cellulase

<400> 26

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Thr Gly Ala Ser Pro Ala Trp Ala Ser Val His Ser Ala Ala Thr His
 -5 -1 1 5

Ala Lys Ala His Val Gly Val Arg Ala Ala Asp Met Ala Ala Ala Ser
 10 15 20

Met Ser Ala Glu Ile Gln Ile Leu His Asp Ala Leu Thr Ala Ser Glu
 25 30 35 40

Leu Ser Ser Val Gln Ala Ala Ala Gln Ala Ala Ala Asn Leu Pro Ala
 45 50 55

Ser Thr Trp Val Ser Trp Leu Tyr Pro Ser Ala Ser Ser Pro Ser Ala
 60 65 70

Ala Gln Thr Gln Thr Ala Gln Ala Leu Gly Ala Leu Leu Thr Leu Val
 75 80 85

Thr Tyr Gly Ala Val Ala Asp Asp Gly Gln Asn Ile Ala Gln Asn Leu
 90 95 100

Gln Thr Leu Gln Ser Thr Ser Pro Leu Leu Ser Pro Ala Ala Val Ser
 105 110 115 120

Met Phe Tyr Gln Asn Phe Phe Val Leu Val Gly Gln Ser Ser Lys Ser
 125 130 135

Val Leu Ser Gly Gln Ala Thr Thr Ser Thr Ala Gly His Ala Leu Ala

140	145	150
Gln Ala Ala Ala Leu Thr Pro Gln Leu Ala Ala Tyr Leu Arg Gln Ser		
155	160	165
Gly Leu Ser Pro Asp Asp Leu Ala Arg Ala Tyr Val Ser Phe Ala Ser		
170	175	180
Ala Val Asp Ser Gln Gly Ala Ala Gln Thr Ala Leu Leu Thr Arg Ile		
185	190	195
Cys Thr Asn Ile Leu Gly Phe Gly Ala Pro Thr Ser Thr Ala Thr Ile		
205	210	215
Thr Val Asn Ala Ala Ala Asn Leu Gly Gln Val Pro Thr Thr Ala Phe		
220	225	230
Gly Leu Asn Ala Ala Val Trp Asp Ser Gly Leu Asn Ser Gln Thr Val		
235	240	245
Ile Ser Glu Val Gln Ala Leu His Pro Ala Leu Ile Arg Trp Pro Gly		
250	255	260
Gly Ser Ile Ser Asp Val Tyr Asn Trp Glu Thr Asn Thr Arg Asn Asp		
265	270	275
Gly Gly Tyr Val Asn Pro Asp Asp Thr Phe Asp His Phe Met Gln Phe		
285	290	295
Val Asn Ala Val Gly Ser Thr Pro Ile Ile Thr Val Asn Tyr Gly Thr		
300	305	310
Gly Thr Pro Gln Leu Ala Ala Asp Trp Val Lys Tyr Ala Asp Val Thr		
315	320	325
His His Asp Asn Val Met Tyr Trp Glu Ile Gly Asn Glu Ile Tyr Gly		
330	335	340
Asn Gly Tyr Tyr Asn Gly Asn Gly Trp Glu Ala Asp Asp His Ala Val		
345	350	355
Ala Gly Gln Pro Gln Lys Gly Asn Pro Gly Leu Ser Pro Gln Ala Tyr		
365	370	375

Ala Gln Asn Ala Leu Gln Phe Ile Lys Ala Met Arg Ala Glu Asp Pro
380 385 390

Ser Ile Lys Ile Gly Ala Val Leu Thr Met Pro Tyr Asn Trp Pro Trp
395 400 405

Gly Ala Thr Val Asn Gly Asn Asp Asp Trp Asn Thr Val Val Leu Lys
410 415 420

Ala Leu Gly Pro Tyr Ile Asp Phe Val Asp Val His Trp Tyr Pro Glu
425 430 435 440

Thr Pro Gly Gln Glu Thr Asp Ala Gly Leu Leu Ala Asp Thr Asp Gln
445 450 455

Ile Pro Ala Met Val Ala Glu Leu Lys Arg Glu Val Asn Thr Tyr Ala
460 465 470

Gly Ser Asn Ala Lys Asn Ile Gln Ile Phe Val Thr Glu Thr Asn Ser
475 480 485

Val Ser Tyr Asn Pro Gly Glu Gln Ser Thr Asn Leu Pro Glu Ala Leu
490 495 500

Phe Leu Ala Asp Asp Leu Thr Gly Phe Ile Gln Ala Gly Ala Ala Asn
505 510 515 520

Val Asp Trp Trp Asp Leu Phe Asn Gly Ala Glu Asp Asn Tyr Thr Ser
525 530 535

Pro Ser Leu Tyr Gly Gln Asn Leu Phe Gly Asp Tyr Gly Leu Leu Ser
540 545 550

Ser Gly Gln Thr Thr Gln Asn Gly Trp Gln Glu Pro Pro Ala Asn Thr
555 560 565

Pro Leu Pro Pro Tyr Asn Gly Phe Gln Leu Val Ser Asp Phe Ala Gln
570 575 580

Pro Gly Asp Thr Met Leu Gly Ser Thr Thr Ser Gln Ser Ala Ile Asp
585 590 595 600

Val His Ala Val Arg Lys Pro Asn Gly Asp Ile Ser Leu Met Leu Val
605 610 615

Asn Arg Ser Pro Ser Ala Ile Tyr Ser Ala Asn Leu Asn Val Leu Gly
620 625 630

Phe Gly Pro Phe Val Val Thr His Ala Leu Ala Tyr Gly Glu Gly Ser
635 640 645

Ser Arg Val Ala Pro Met Pro Val Leu Pro Val Pro Gly Ala Pro Ile
650 655 660

Lys Leu Met Pro Tyr Ser Gly Ile Asp Leu Thr Leu His Pro Leu Ile
665 670 675 680

Pro Ala Pro His Ala Ala Ala Gln Val Thr Asp Thr Leu Thr Leu Ser
685 690 695

Ser Pro Thr Val Thr Ala Gly Gly Ala Glu Thr Leu Ser Ala Ser Phe
700 705 710

Gln Ala Asp Arg Pro Val His His Ala Thr Val Glu Leu Glu Leu Tyr
715 720 725

Asp Ser Thr Asn Asp Leu Val Ala Thr His Thr Val Ser Asp Val Asp
730 735 740

Leu Gln Pro Gly Ser Ala Thr Ser Glu Thr Trp Ser Phe Thr Ala Pro
745 750 755 760

Ala Ala Asn Gly Asn Tyr Arg Val Glu Ala Phe Val Phe Asp Pro Val
765 770 775

Thr Gly Ala Thr Tyr Asp Ala Asp Thr Gln Gly Ala Val Leu Thr Val
780 785 790

Asn Gln Pro Pro Gln Ala Thr Tyr Gly Asp Ile Val Thr Lys Asp Thr
795 800 805

Val Ile Thr Val Asn Gly Thr Thr Tyr Asp Val Pro Ala Pro Asp Ala
810 815 820

Gly Gly His Tyr Pro Ser Gly Thr Asn Ile Ser Val Ala Pro Gly Asp
825 830 835 840

Thr Val Thr Val Gln Thr Thr Phe Val Asn Val Ser Ser Thr Asp Ala
845 850 855

Leu Gln Asn Gly Leu Ile Asp Met Glu Val Asp Gly Ser Asn Gly Ala
860 865 870

Ile Leu Gln Lys Tyr Trp Pro Ser Thr Thr Leu Leu Pro Gly Gln Ser
875 880 885

Glu Thr Val Thr Ala Thr Trp Gln Val Pro Ala Asn Val Ala Ala Gly
890 895 900

Thr Tyr Pro Leu Asn Phe Gln Ala Phe Asn Thr Ser Ser Trp Thr Gly
905 910 915 920

Asn Cys Tyr Phe Thr Asn Gly Gly Val Val Asn Phe Val Ile Ser
925 930 935

<210> 27
<211> 272
<212> PRT
<213> Alicyclobacillus sp.

<220>
<221> SIGNAL
<222> (1)..(32)

<220>
<221> mat_peptide
<222> (33)..(272)
<223> aspartyl protease

<400> 27

Met Asn Gly Thr Ser Val Trp Lys Ala Ser Gly Ile Ala Ala Ala Ser
-30 -25 -20

Cys Leu Thr Ala Ala Ala Leu Leu Ala Trp Pro His Ala Thr Ser Thr
-15 -10 -5 -1

Leu Asp Ala Ser Pro Ala Ile Phe His Ala Pro Arg His Ala Leu Ser
1 5 10 15

Pro Asn Thr Ser Pro Lys Pro Asn Ser Val Gln Ala Gln Asn Phe Gly
 20 25 30
 Trp Ser Ala Ser Asn Trp Ser Gly Tyr Ala Val Thr Gly Ser Thr Tyr
 35 40 45
 Asn Asp Ile Thr Gly Ser Trp Ile Val Pro Ala Val Ser Pro Ser Lys
 50 55 60
 Arg Ser Thr Tyr Ser Ser Ser Trp Ile Gly Ile Asp Gly Phe Asn Asn
 65 70 75 80
 Ser Asp Leu Ile Gln Thr Gly Thr Glu Gln Asp Tyr Val Asn Gly His
 85 90 95
 Ala Gln Tyr Asp Ala Trp Trp Glu Ile Leu Pro Ala Pro Glu Thr Val
 100 105 110
 Ile Ser Asn Met Thr Ile Ala Pro Gly Asp Arg Met Ser Ala His Ile
 115 120 125
 His Asn Asn Gly Asn Gly Thr Trp Thr Ile Thr Leu Thr Asp Val Thr
 130 135 140
 Arg Asn Glu Thr Phe Ser Thr Thr Gln Ser Tyr Ser Gly Pro Gly Ser
 145 150 155 160
 Ser Ala Glu Trp Ile Gln Glu Ala Pro Glu Ile Gly Gly Arg Ile Ala
 165 170 175
 Thr Leu Ala Asn Tyr Gly Glu Thr Thr Phe Asp Pro Gly Thr Val Asn
 180 185 190
 Gly Gly Asn Pro Gly Phe Thr Leu Ser Asp Ala Gly Tyr Met Val Gln
 195 200 205
 Asn Asn Ala Val Val Ser Val Pro Ser Ala Pro Asp Ser Asp Thr Asp
 210 215 220
 Gly Phe Asn Val Ala Tyr Gly Ser Asn Gln Pro Ser Pro Pro Ala Ser
 225 230 235 240

<210> 28

<211> 315
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(25)

<220>
 <221> mat_peptide
 <222> (26)..(315)
 <223> multi copper oxidase

<400> 28

Met Arg Arg Arg Met Ser Gly Phe Ala Thr Gly Leu Gly Ile Ala Ala
 -25 -20 -15 -10

Gly Leu Ala Leu Ser Ser Ala Leu Ala Ala Pro Phe Phe His Ala Gly
 -5 -1 1 5

Asn Ala Ser Ala Ala Ser Thr Met Ser Met Ala Pro Thr Ser Thr Met
 10 15 20

Gly Ala Leu Pro Ala Pro Glu Gly Val Pro Asp Ala Gly Pro Leu Ser
 25 30 35

Ile Thr Pro Glu Val Ile Arg Gln Gln Gln Ala Asp Ala Val Arg Val
 40 45 50 55

Met Asp Glu Glu Gly Leu Lys Pro Gln Ile Leu Ser Gly Asp Ile Lys
 60 65 70

Arg Phe Thr Leu Thr Ala Ser Gln Val Asn Trp Tyr Leu Tyr Pro Gly
 75 80 85

Lys Ala Val Val Ala Cys Gly Tyr Asn Gly Gln Val Pro Gly Pro Val
 90 95 100

Leu Arg Val Arg Val Gly Asp Arg Val Gln Ile Leu Leu Arg Asn Glu
 105 110 115

Leu Asn Glu Pro Thr Thr Leu His Ile Gln Gly Leu Asp Leu Pro Ala
 120 125 130 135

Ser Gln Leu Gly Ile Gly Asp Val Thr Glu Ser Pro Ile Pro Pro Gly

<400> 29

Met Gly Leu Trp Lys Arg Leu Ala Leu Gly Val Pro Ala Ala Leu
-185 -180 -175

Ser Met Leu Ala Val Gly Val Pro Val Met Ser Ala Asp Thr Val
-170 -165 -160

Glu Ala Ala Pro Leu Ala Asn Pro Ser Thr Glu Asn Ala Gln Asp
-155 -150 -145

Met Gly Pro Ala Ser Gly Ser Gln Thr Val Thr Ala Ser Ile Ile
-140 -135 -130

Leu Arg Val Gln Asn Pro Thr Ala Leu Gln Asn Tyr Ile Gln Glu
-125 -120 -115

Thr Glu Thr Pro Gly Ser Pro Leu Tyr His Lys Phe Leu Thr Thr
-110 -105 -100

Ala Gln Phe Ala Gln Gln Tyr Ala Pro Ser Ala Ala Thr Leu Gln Gln
-95 -90 -85

Ile Glu Gln Glu Leu Gln Gly Tyr Gly Leu Gln Val Val Asn Val Asp
-80 -75 -70

Ala Asp His Leu Asp Met Gln Val Gln Gly Thr Val Gln Gln Phe Asp
-65 -60 -55

Asn Ala Phe Asn Thr Val Ile Asp Leu Phe Lys Ala Asn Gly His Ile
-50 -45 -40

Phe Arg Ala Pro Lys Lys Pro Pro Gln Ile Pro Val Ala Leu Leu Thr
-35 -30 -25 -20

Asn Val Leu Ala Val Val Gly Leu Asp Thr Ala Gln Ala Ala Gln Ser
-15 -10 -5

Leu Thr Val Lys Thr Pro Asn Val Ala Gly Val Pro Ser Pro Lys Val
-1 1 5 10

Val Leu Pro Gln Gly Gly Ser Thr Ala Thr Gly Thr Pro Gly Ser Tyr
15 20 25

Thr Val Gly Asp Thr Ala Asn Arg Tyr Asp Ile Asn Pro Leu Tyr Gln
 30 35 40 45
 Lys Gly Ile Thr Gly Lys Gly Glu Thr Ile Gly Ile Val Thr Leu Ser
 50 55 60
 Ser Phe Asn Pro Gln Asp Ala Tyr Thr Tyr Trp Gln Gly Ile Gly Leu
 65 70 75
 Lys Val Ala Pro Asn Arg Ile Gln Met Val Asn Val Asp Gly Gly Gly
 80 85 90
 Gln Met Asp Asp Gly Ser Val Glu Thr Thr Leu Asp Val Glu Gln Ser
 95 100 105
 Gly Gly Leu Ala Pro Asp Ala Asn Val Val Val Tyr Asp Ala Pro Asn
 110 115 120 125
 Thr Asp Gln Gly Phe Ile Asp Ala Phe Tyr Gln Ala Val Ser Asp Asn
 130 135 140
 Gln Ala Asp Ser Leu Ser Val Ser Trp Gly Gln Pro Glu Ile Asp Tyr
 145 150 155
 Leu Pro Gln Met Asn Gln Gly Gln Ser Tyr Val Asp Glu Leu Leu Ala
 160 165 170
 Phe Thr Gln Ala Phe Met Glu Ala Ala Ala Gln Gly Ile Ser Met Tyr
 175 180 185
 Ala Ala Ala Gly Asp Ser Gly Ala Tyr Asp Thr Ala Arg Asp Phe Pro
 190 195 200 205
 Pro Ser Asp Gly Phe Thr Thr Pro Leu Ser Val Asp Phe Pro Ala Ser
 210 215 220
 Asp Pro Tyr Ile Thr Ala Ala Gly Gly Thr Thr Val Pro Phe Thr Ala
 225 230 235
 Lys Phe Ser Leu Gly Thr Val Asn Ile Thr Gln Glu Gln Pro Trp Ser
 240 245 250

Trp Gln Tyr Leu Gln Asn Leu Gly Tyr Gln Gly Leu Phe Ser Val Gly
 255 260 265

Thr Gly Gly Gly Val Ser Val Ile Phe Pro Arg Pro Trp Tyr Gln Leu
 270 275 280 285

Gly Val Gly Gly Met Gln Asn Ser Ala Ala Asn Gln Ala Phe Thr Asp
 290 295 300

Ser Gln Gly Val Leu Tyr Gly Ser Pro Phe Thr Tyr Asn Leu Pro Ser
 305 310 315

Asn Tyr Ala Gly Arg Asn Leu Pro Asp Ile Ser Met Asp Ala Asp Pro
 320 325 330

Glu Thr Gly Tyr Leu Val Tyr Trp Ser Ala Gly Gly Gly Trp Ile Ala
 335 340 345

Gly Tyr Gly Gly Thr Ser Phe Val Ala Pro Gln Leu Asn Gly Ile Thr
 350 355 360 365

Ala Leu Ile Asp Gln Glu Val His Gly Arg Val Gly Phe Leu Asn Pro
 370 375 380

Leu Leu Tyr Thr Leu Leu Thr Gln Gly Val Gln Gly Gly Ala Gln Pro
 385 390 395

Phe His Asp Ile Thr Thr Gly Asn Asn Trp Tyr Trp Asn Ala Val Pro
 400 405 410

Gly Tyr Asp Pro Ala Ser Gly Val Gly Thr Pro Asp Val Ala Asn Leu
 415 420 425

Ala Gln Asp Ile Ala Ser Leu Arg
 430 435

<210> 30
 <211> 533
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL

<222> (1) .. (24)

<220>

<221> mat_peptide

<222> (25) .. (534)

<223> serine-carboxyl protease

<400> 30

Met Arg Ala Leu Ala His Leu Ala Ile Gly Ala Ile Ala Ser Gly Val
-20 -15 -10

Phe Ala Ala Pro Val Ala Phe Ala Ser Pro Val Gln Glu Arg Val Val
-5 -1 1 5

Val Ala Ser Pro Asp Pro Arg Thr Arg Ser Val His Ala Asp Gly Glu
10 15 20

Ile Ser Pro Ser Gln Pro Met His Leu Val Ile Thr Leu Arg Leu Arg
25 30 35 40

His Glu Ala Gln Leu Glu Gln Leu Ile Arg Asp Leu Tyr Thr Pro Gly
45 50 55

Ser Pro Asp Ala Gly His Phe Leu Thr Pro Ala Ala Phe Asn Ala Ala
60 65 70

Tyr Ala Pro Thr Ala Glu Asp Val Gln Ala Val Val Gln Gly Leu Arg
75 80 85

Ala Tyr Gly Leu Arg Val Glu Pro Thr Val Asn Pro Met Val Leu Thr
90 95 100

Val Ser Gly Arg Ala Arg Asp Val Glu Arg Ala Phe Gly Val His Glu
105 110 115 120

Leu Gln Phe Gly Arg Gly Ala Gly Ala Trp Tyr Ala Pro Asp Gly Ala
125 130 135

Ala Thr Leu Pro Ala Pro Leu Ala Ala Arg Val Ser Ala Val Val Gly
140 145 150

Leu Thr Ser Asp Ala Met Glu Arg His Leu Val Leu Ala His Val Ala
155 160 165

Pro Ala Gly Gly Gly Tyr Thr Pro Ala Gln Ile Gln Arg Ala Tyr Asp
 170 175 180

Tyr Thr Pro Leu Tyr Ser Gln Tyr Met Gly Arg Gly Gln Val Ile Ala
 185 190 195 200

Val Val Thr Ser Gly Ser Val Leu Arg Ser Asp Leu Leu Ala Phe Asp
 205 210 215

Arg Ala Phe Gly Leu Pro Asn Pro Val Val Arg Gln Arg Val Ile Asp
 220 225 230

Gly Ser Ser Thr Ser Pro Asp Asp Glu Thr Thr Leu Asp Cys Glu Trp
 235 240 245

Ala His Ala Ile Ala Pro Thr Ala Ser Leu Ala Val Tyr Glu Ala Ala
 250 255 260

Gln Pro Asp Ala Gln Ser Phe Ile Asp Ala Phe Ala Gln Val Ala Ala
 265 270 275 280

Asp Asp Gly Ala His Val Val Thr Thr Ser Trp Gly Ala Pro Glu Ser
 285 290 295

Glu Thr Asp Ala Ala Thr Met Gln Ala Glu His Gln Ile Phe Met Gln
 300 305 310

Met Ala Ala Gln Gly Gln Ser Val Phe Ala Ala Ala Gly Asp Ser Gly
 315 320 325

Ser Ser Asp Gly Thr Ser Gly Thr Asp Val Asp Tyr Pro Ser Ser Asp
 330 335 340

Pro Tyr Val Thr Ala Cys Gly Gly Thr Arg Leu Val Leu Gly Ala Gly
 345 350 355 360

Ala Lys Arg Leu Gln Glu Thr Ala Trp Ala Asp Thr Gly Gly Gly Ala
 365 370 375

Ser Ser Val Tyr Gly Glu Pro Trp Trp Gln Tyr Gly Pro Gly Val Pro
 380 385 390

Gln Thr Gly Tyr Arg Gln Thr Cys Asp Val Ala Leu Asn Ala Asp Pro

395 400 405
 Ala Thr Gly Tyr Asp Phe Ile Tyr Glu Gly Gln Trp Glu Val Ala Gly
 410 415 420

 Gly Thr Ser Phe Val Ala Pro Met Met Ala Ala Thr Phe Ala Leu Ile
 425 430 435 440

 Asp Gln Ala Arg Ala Leu Glu Gly Lys Pro Pro Val Gly Leu Ala Asp
 445 450 455

 Val Gly Ile Tyr Ala Met Ala Arg Asn Ala Ser Tyr Ala Pro Tyr Ala
 460 465 470

 Phe His Asp Ile Thr Ala Gly Ser Asn Gly Ala Tyr Ser Ala Gly Pro
 475 480 485

 Gly Trp Asp His Pro Thr Gly Phe Gly Ser Ile Asp Ala Tyr Tyr Phe
 490 495 500

 Leu His Gly Leu Asp
 505

 <210> 31
 <211> 360
 <212> PRT
 <213> Alicyclobacillus sp.

 <220>
 <221> SIGNAL
 <222> (1)..(41)

 <220>
 <221> mat_peptide
 <222> (42)..(411)
 <223> protease or a HtrA-like serine protease

 <400> 31

 Met Arg Arg Arg Arg Trp Asp Tyr Glu Asp Trp Pro Ser Glu Asn Arg
 -40 -35 -30

 Arg Val Gly Val Trp Leu Ala Ser Gly Thr Ala Leu Leu Ala Ile Cys
 -25 -20 -15 -10

 Tyr Ile Leu Gly Ile Trp Thr Gly Ala Ala Leu Thr Arg Gly His Ser

-5

-1 1

5

Gln Thr Thr Val Glu Tyr Val Pro Pro Gln Thr Gly Asn Thr Ala Ser
10 15 20

Thr Ser Gly Ser Leu Thr Pro Ile Pro Gly Val Glu Asp Thr Thr Ile
25 30 35

Val Thr Gln Ile Tyr Asn Arg Val Lys Asn Ser Ile Phe Thr Ile Thr
40 45 50 55

Ala Val Ser Gly Gly Lys Pro Thr Ser Ser Asp Ala Glu Glu Asp Ile
60 65 70

Gly Thr Gly Phe Leu Ile Asp His Asn Gly Asp Leu Leu Thr Asn Ala
75 80 85

His Val Val Gly Ser Ala Thr Thr Val Gln Val Ser Gly Asp Asn Arg
90 95 100

Gln Phe Val Gly Arg Val Ile Asp Ala Asp Gln Leu Asp Asp Leu Ala
105 110 115

Ile Val Arg Ile Pro Ala Pro Lys Ser Leu Glu Pro Leu Pro Leu Gly
120 125 130 135

Ser Val Lys Ser Leu Gln Pro Gly Ser Leu Val Ile Ala Ile Gly Asn
140 145 150

Pro Phe Glu Leu Thr Ser Ser Val Ser Ser Gly Ile Val Ser Gly Leu
155 160 165

Asn Arg Ser Met Ser Glu Ser Asn Gly His Val Met Asn Gly Met Ile
170 175 180

Gln Thr Asp Ala Pro Leu Asn Pro Gly Asn Ser Gly Gly Pro Leu Leu
185 190 195

Asn Ala Ala Gly Gln Val Val Gly Ile Asn Thr Leu Ile Glu Ser Pro
200 205 210 215

Ile Glu Gly Ser Ile Gly Ile Gly Phe Ala Ile Pro Ile Asp Arg Phe
220 225 230

Ile Gln Leu Glu Pro Glu Leu Leu Ala Gly Lys Pro Val Ala His Ala
 235 240 245

Trp Leu Gly Ile Glu Gly Met Asp Ile Asp Asn Leu Met Arg Gln Ala
 250 255 260

Leu His Leu Pro Val Ala Ser Gly Val Tyr Val Thr Glu Val Thr Pro
 265 270 275

Gly Gly Pro Ala Ala Lys Ala Gly Leu Arg Gly Asp Ser Asn Ala Ala
 280 285 290 295

Lys Leu Asn Ser Leu Ser Gln Ser Ala Asn Pro Tyr Ala Leu Leu Lys
 300 305 310

Gly Asn Gly Asp Ile Ile Val Gly
 315

<210> 32
 <211> 211
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(30)

<220>
 <221> mat_peptide
 <222> (31)..(212)
 <223> disulfide isomerase

<400> 32

Met Arg Arg Ser Trp Ser Val Leu Met Ala Val Cys Met Ser Trp Leu
 -30 -25 -20 -15

Ala Val Gly Cys Gly Thr Pro Ala Asn Ser Leu Ser Gln Ala Thr Ala
 -10 -5 -1 1

Ala Ser Gly Arg His Ala Pro His Pro Leu Val Phe Gln Asn Leu Thr
 5 10 15

Gly Ala Met Asn Glu Gly Gln Asp Pro Arg Trp Asp Pro Lys Ala Ala
 20 25 30

Pro Thr Gly Val Tyr Asp Asp Val Thr Val Val Thr Ala Ser Gly Arg
 35 40 45 50
 Gln Glu Val Leu Ser Val Arg Asp Ala Pro Leu Leu Phe Ala Ala Tyr
 55 60 65
 Trp Cys Pro His Cys Gln Arg Thr Leu Gln Leu Leu Thr Ser Ile Glu
 70 75 80
 Ser Arg Leu Lys Gln Lys Pro Ile Leu Val Asn Val Gly Tyr Pro Pro
 85 90 95
 Gly Thr Thr Leu Gln Thr Ala Ala Arg Ile Ala Arg Glu Glu Ser Gln
 100 105 110
 Val Leu His Leu Ala Pro Phe Gln Glu Val Phe Ile Leu Asn Pro Asp
 115 120 125 130
 Ala Gly Asp Arg Tyr Ala Pro Leu Gly Tyr Pro Thr Leu Ala Phe Tyr
 135 140 145
 Arg Ala Gly Arg Asp Trp Thr Leu Tyr Gly Glu His Arg Ala Ser Ile
 150 155 160
 Trp Glu Lys Ala Leu Ser Glu Ser Thr Ser Lys Ala Tyr Asn Gly Ser
 165 170 175
 Glu Glu Ser
 180

<210> 33
 <211> 266
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(29)

<220>
 <221> mat_peptide
 <222> (30)..(266)
 <223> gamma-D-glutamyl-L-diamino acid endopeptidase

<400> 33

Met Asp Glu Met Asn Ile Arg Ser Trp Cys Val Ala Ala Cys Thr Val
-25 -20 -15

Ala Leu Thr Ser Ala Val Gly Ala Thr Thr Ala Phe Ala Gln Thr Val
-10 -5 -1 1

Thr Val Gln Pro Gly Gln Ser Leu Trp Thr Ile Ala Arg Ala His Gly
5 10 15

Met Pro Val Gln Leu Val Ala Ser Ala Asn Pro Gln Tyr Asn Pro Leu
20 25 30 35

Asn Leu Pro Val Gly Ala Thr Val Thr Leu Pro Ser Leu Lys Asp Val
40 45 50

Ala Val Gln Pro Gly Asp Ser Leu Phe Leu Ile Gly Arg Gln Tyr Gly
55 60 65

Val Ser Leu Ala Glu Met Leu Ala Ala Asn Pro Asn Val Asp Pro Leu
70 75 80

Asn Leu Gln Val Gly Ser Ser Val Arg Val Pro Leu Ala Ser Ser Ser
85 90 95

Thr Lys Ser Ser Thr Val Ser Ala His Val Ala Ala Ser Thr Pro Glu
100 105 110 115

Asn Ser Asn Asn Leu Tyr Trp Leu Glu Arg Val Ile His Ala Glu Ala
120 125 130

Gly Gly Glu Ser Leu Gln Ala Gln Ile Ala Val Ala Asp Val Ile Leu
135 140 145

His Arg Met Ala Ala Gly Gly Tyr Gly Ser Thr Val Gln Gln Val Val
150 155 160

Phe Gln Val Ser Asp Gly His Tyr Gln Phe Glu Ser Val Ala Asn Gly
165 170 175

Ser Ile Tyr Gly Gln Pro Asp Ala Gln Asn Val Gln Ala Ala Leu Asp
180 185 190 195

Ala Leu Asn Gly Asp Asp Val Val Pro Gly Ala Leu Val Phe Tyr Asn
200 205 210

Pro Ala Gln Thr Pro Ser Gly Ser Trp Val Trp Gln Gln Pro Val Val
215 220 225

Ala His Ile Gly His Leu Val Phe Ala Lys
230 235

<210> 34
<211> 768
<212> PRT
<213> Alicyclobacillus sp.

<220>
<221> SIGNAL
<222> (1)..(26)

<220>
<221> mat_peptide
<222> (27)..(768)
<223> endo-beta-N-acetylglucosaminidase

<400> 34

Met Lys Thr His Arg Leu Leu Ala Val Ala Ala Leu Pro Ala Thr Val
-25 -20 -15

Leu Leu Thr Thr Pro Ala Pro Ala Leu Ala Glu Thr Ser Ser Ser Gln
-10 -5 -1 1 5

Ser Ala Ser Ala Pro Ser Leu Asn Val Pro Val Ala Ala Leu Thr Leu
10 15 20

Ala Gly Val Gln Ser Tyr Pro Met Leu Ser Tyr Gly Ser Thr Gly Val
25 30 35

Tyr Val Glu Ile Leu Gln Asn Ala Leu Asn Ala Leu Gly Tyr Asp Val
40 45 50

Gly Gln Ala Ser Gly Leu Phe Asp Ala Thr Thr Gln Ala Glu Val Lys
55 60 65 70

Ala Phe Gln Gln Ala Met Gly Leu Gln Thr Asp Gly Ile Val Gly Pro
75 80 85

Leu Thr Trp Gly Ala Leu Ala Lys Ala Val Ala Asp Tyr Arg Gln Val
 90 95 100

Met Thr Val Leu Ser Ser Arg Ser Ser Leu Val Gln Gln Val Glu Trp
 105 110 115

Lys Arg Ile Val Trp Asn Gly Arg Leu Ile Ser Lys Pro Ile Gly Phe
 120 125 130

Thr Tyr Gln Gly Thr Ala Tyr Met Pro Ile Trp Tyr Val Met Gln Ala
 135 140 145 150

Leu Ser Lys Ala Gly Ile Ala Ser Thr Trp Gln Gly Gly Val Trp Thr
 155 160 165

Leu Thr Pro Pro Gly Gly Gln Thr Val Asn Tyr Gly Lys Ile Ser Tyr
 170 175 180

Gly Pro Gly Ser Ala Ala Ile Ala Ile Gly Gln Thr Val Val Ala Asn
 185 190 195

Val Pro Ala Val Val Tyr Pro Asp Pro Ala Ser Gly Lys Leu Thr Thr
 200 205 210

Phe Met Pro Val Trp Tyr Val Met Asn Ala Leu Gln Arg Leu Gly Ile
 215 220 225 230

Gly Ser Thr Trp Gln Gly Thr Glu Trp Asp Met Lys Pro Ala Pro Val
 235 240 245

Val Ile Glu Thr Gly Asp Pro Ser Asn Asn Thr Thr Gly Ser Asp Pro
 250 255 260

Ala Asn Ser Thr Gly Asn Gly Thr Gly Asn Ser Thr Gly Asn Ala Thr
 265 270 275

Gly Ala Val Pro Gly Gly Asn Thr Val Thr Asn Val Thr Thr Gly Ser
 280 285 290

Ser Asn Val Thr Gly Asn Ser Thr Gly Asn Ser Leu Gly Asn Ser Thr
 295 300 305 310

Gly Asn Ser Leu Gly Asn Ser Thr Ser Asn Ala Thr Gly Asn Ala Thr
 315 320 325

Gly Asn Thr Thr Gly Asn Ala Thr Gly Asn Ser Thr Gly Thr Ser Ser
 330 335 340

Gly Ser Phe Thr Asn Val Asp Leu Arg Tyr Pro Ala Pro Ser Asn Ile
 345 350 355

Asn Ala Gln Ser Ile Asn Gln Phe Leu Leu Gln Asn Ser Ser Pro Leu
 360 365 370

Asn Gly Leu Gly Asn Ser Phe Met Asp Ala Gln Asn Leu Tyr Ser Val
 375 380 385 390

Asp Ala Asn Tyr Leu Val Ser His Ala Ile Leu Glu Ser Ala Trp Gly
 395 400 405

Gln Ser Gln Ile Ala Leu Gln Lys Asn Asn Leu Phe Gly Tyr Gly Ala
 410 415 420

Tyr Asp Ser Asn Pro Gly Gln Asp Ala Gly Val Phe Pro Ser Asp Asp
 425 430 435

Tyr Ala Ile Arg Phe Glu Ala Trp Thr Val Arg Met Asn Tyr Leu Thr
 440 445 450

Pro Gly Ala Ser Leu Tyr Val Thr Pro Thr Leu Ser Gly Met Asn Val
 455 460 465 470

Asn Tyr Ala Thr Ala Lys Thr Trp Ala Ser Gly Ile Ala Ala Ile Met
 475 480 485

Thr Gln Phe Ala Ser Ser Val Gly Ser Asn Val Asn Ala Tyr Val Gln
 490 495 500

Tyr Thr Pro Ser Asn Asn Pro Pro Ala Pro Arg Ser Thr Ala Glu Pro
 505 510 515

Val Tyr Tyr Met Asn Gly Ala Gln Gly Val Thr Gln Gln Asp Pro Tyr
 520 525 530

Tyr Pro Asn Gly Gly Val Pro Tyr Tyr Pro Thr Ile Ala Gln Gly Glu

535		540		545		550
Asn Gln Gln Phe Phe Gly Gln Leu Ser Val Gly Ser Phe Gly Gln Pro						
		555		560		565
Val Val Glu Val Gln Gln Phe Leu Asn Arg Thr Ile Asn Ala Gly Leu						
		570		575		580
Thr Val Asp Gly Gln Phe Gly Pro Leu Thr Gln Ala Ala Val Glu Lys						
		585		590		595
Phe Gln Ser Gln Val Met His Met Ser Asn Pro Asn Gly Ile Trp Thr						
		600		605		610
Phe Ser Met Trp Val Gln Tyr Ile Gln Pro Ser Gln Ser Asn Ala Asn						
		615		620		625
						630
Leu Ile Pro Ala Gly Thr Thr Val Lys Ile Asp Gln Val Ala Glu Gly						
		635		640		645
Met Ala Gly Pro Tyr Val Val Pro Trp Tyr His Val Val Gly Tyr Gly						
		650		655		660
Trp Val Asp Ser Gln Tyr Ile Lys Leu Thr Asn Val Tyr Arg Val Ile						
		665		670		675
Val Gln Asn Pro Ala Gly Thr Ala Thr Thr Ile Pro Val Tyr Gln Val						
		680		685		690
Gly Asn Leu Ser Ser Val Leu Leu Asn Leu His Ser Gly Asp Trp Val						
		695		700		705
						710
Val Ala Asn Ser Ala Gln Pro Ser Gly Gly Val Tyr Thr Ile Gln Ile						
		715		720		725
Ala Ala Gln Asp Pro Pro Cys Arg Thr Ala Thr Pro Pro Gly Arg Ser						
		730		735		740

<210> 35
 <211> 597
 <212> PRT
 <213> Alicyclobacillus sp.

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<220>
<221> SIGNAL
<222> (1)..(49)

<220>
<221> mat_peptide
<222> (50)..(597)
<223> multi copper oxidase

<220>
<221> MISC_FEATURE
<222> (139)..(139)
<223> putative copper binding site

<220>
<221> MISC_FEATURE
<222> (141)..(141)
<223> putative copper binding site

<220>
<221> MISC_FEATURE
<222> (181)..(181)
<223> putative copper binding site

<220>
<221> MISC_FEATURE
<222> (183)..(183)
<223> putative copper binding site

<220>
<221> MISC_FEATURE
<222> (514)..(514)
<223> putative copper binding site

<220>
<221> MISC_FEATURE
<222> (566)..(566)
<223> putative copper binding site

<400> 35

Met Met Ala His Asp Arg Leu Asp Arg Arg Val Asn Glu Arg Arg Gln
          -45                      -40                      -35

Ala Met Arg Arg Ala Ala Lys Trp Ala Ile Ala Leu Gly Thr Thr Ala
          -30                      -25                      -20

Val Val Ala Gly Val Ser Ser Val Phe Ala Leu Arg Ser Val Arg Glu
          -15                      -10                      -5

Ala Asn Leu Asn Pro Asn Ala Pro Leu Ala Asn Val Pro Gly Pro Gln
-1  1                      5                      10                      15

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Gly Ala Tyr Thr Pro Ile Ser Ala Leu Gln Pro Val Val Pro Lys Asn
 20 25 30

Ala Arg Ile Asp His Tyr Thr Leu Thr Ala Glu Ser Arg Thr Leu Thr
 35 40 45

Val Gly Gly His Ala Leu Gln Ala Met Thr Phe Asn Gly Thr Ala Pro
 50 55 60

Gly Pro Leu Leu Val Ala His Gln Gly Asp Val Val Lys Val Thr Val
 65 70 75

His Asn Arg Leu Ser Val Pro Leu Thr Ile His Trp His Gly Ile Ala
 80 85 90 95

Val Pro Gly Ala Glu Asp Gly Val Pro Gly Val Thr Gln Asn Pro Ile
 100 105 110

Pro Pro Gly Gly Ser Tyr Thr Tyr Glu Phe Gln Val Asn Gln Pro Gly
 115 120 125

Thr Tyr Trp Tyr His Ser His Glu Ala Ser Phe Glu Glu Val Gly Leu
 130 135 140

Gly Leu Tyr Gly Ala Phe Val Val Leu Pro Lys Arg Ala Val His Pro
 145 150 155

Ala Asp Arg Asp Tyr Thr Leu Val Leu His Glu Trp Pro Thr Ala Ser
 160 165 170 175

Thr Ala Gln Thr Met Met Ala Asn Leu Lys Ala Gly Asn Leu Gly Phe
 180 185 190

Ser Ala Lys Gly Glu Ser Ala Gly Met Gly Gly Met Gly Met Gln Gln
 195 200 205

Asn Gly Asp Met Asn Gly Met Gly Met Met Gly Ala Ala Asp Gly Thr
 210 215 220

Gly Gln Gly Gly Asn Ser Ala Ser Asp Ile Ala His Val Leu Pro Gly
 225 230 235

Pro Pro Leu Gln Leu Asn Gly Phe Ser Pro Thr Ala Asn Asp Trp Ala

240		245		250		255									
Ala	Leu	Asp	Glu	Met	Ala	Gly	Met	Tyr	Asp	Ala	Phe	Thr	Val	Asn	Gln
			260						265					270	
Asn	Ala	Ser	Gly	Thr	Thr	Leu	Leu	Pro	Ala	Lys	Pro	Gly	Gln	Leu	Val
			275					280					285		
Arg	Leu	Arg	Ile	Val	Asn	Ser	Gly	Asn	Met	Thr	His	Leu	Phe	Thr	Leu
		290					295					300			
Val	Gly	Ala	Pro	Phe	Arg	Val	Val	Ala	Leu	Asp	Gly	His	Asp	Ile	Ala
	305					310					315				
Asn	Pro	Gly	Trp	Ile	Arg	Gly	Val	Leu	Leu	Pro	Val	Gly	Ala	Ala	Glu
320					325					330					335
Arg	Tyr	Asp	Ile	Glu	Phe	Arg	Val	Pro	Lys	Ser	Gly	Ala	Ala	Phe	Leu
			340						345					350	
Val	Cys	Ala	Asp	Pro	Asp	Thr	Thr	Ala	Gln	Arg	Glu	Leu	Arg	Ala	Ala
			355					360					365		
Ile	Gly	Leu	Pro	Asp	Ala	Trp	Ser	Gln	Phe	Lys	Glu	Thr	Asp	Ala	Ala
		370					375					380			
Ser	Leu	Glu	Arg	Ala	Pro	Trp	Phe	Asp	Phe	Thr	His	Tyr	Gly	Ser	Gly
	385					390					395				
Arg	Leu	Pro	Gly	Glu	Ala	Val	Phe	Arg	Leu	His	Gln	Ala	Tyr	Gln	Val
400					405					410					415
Arg	Tyr	Asn	Met	Lys	Leu	Thr	Val	Gly	Met	Ser	Met	Asn	Gly	Met	Val
				420					425					430	
Tyr	Ala	Ile	Asn	Gly	Lys	Val	Phe	Pro	Asn	Ile	Pro	Pro	Ile	Val	Val
			435					440					445		
Arg	Lys	Gly	Asp	Ala	Val	Leu	Val	His	Ile	Val	Asn	Asp	Ser	Pro	Tyr
		450						455				460			
Ile	His	Pro	Met	His	Leu	His	Gly	His	Asp	Phe	Gln	Val	Leu	Thr	Arg
	465					470					475				

Asp Gly Lys Pro Val Ser Gly Ser Pro Ile Phe Leu Asp Thr Leu Asp
 480 485 490 495

Val Phe Pro Gly Glu Ser Tyr Asp Ile Ala Phe Arg Ala Asp Asn Pro
 500 505 510

Gly Leu Trp Met Phe His Cys His Asp Leu Glu His Ala Ala Ala Gly
 515 520 525

Met Asp Val Met Val Gln Tyr Ala Gly Ile Arg Asp Pro Tyr Pro Met
 530 535 540

Ser Glu Met Ser Glu
 545

<210> 36
 <211> 245
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(29)

<220>
 <221> mat_peptide
 <222> (30)..(246)
 <223> peptidyl-prolyl-isomerase

<400> 36

Met Lys Arg Arg Thr Leu Leu Ala Gly Ile Thr Leu Ala Ala Leu Val
 -25 -20 -15

Ala Val Ala Gly Cys Gly Thr Pro Ala Gly Asn Thr Ala Ser Pro Asp
 -10 -5 -1 1

Asn Thr Ala Asn Leu Ser Asn Thr Asn Ala Pro Asp Thr Leu Ser Asn
 5 10 15

Glu Thr Gly Gln Thr Leu Asp Thr Ala Asn Pro Pro Tyr Leu His Thr
 20 25 30 35

Ser Thr Glu Gln Trp Lys Ser Met Pro Lys Met Phe Ile Asn Pro Asn
 40 45 50

Lys Thr Tyr Asp Ala Ile Val His Thr Asn Tyr Gly Thr Phe Thr Ile
55 60 65

Gln Leu Phe Ala Lys Asp Ala Pro Ile Thr Val Asn Asn Phe Val Phe
70 75 80

Leu Ala Glu His Asn Phe Tyr His Asp Cys Thr Phe Phe Arg Ile Val
85 90 95

Lys Asn Phe Val Ile Gln Thr Gly Asp Pro Arg Asn Asp Gly Thr Gly
100 105 110 115

Gly Pro Gly Tyr Thr Ile Pro Asp Glu Leu Ser His Gln Val Pro Phe
120 125 130

Thr Lys Gly Ile Val Ala Met Ala Asn Thr Gly Gln Pro His Thr Gly
135 140 145

Gly Ser Gln Phe Phe Ile Cys Thr Ala Asn Asp Thr Gln Val Phe Gln
150 155 160

Pro Pro Asn Asn Arg Tyr Thr Glu Phe Gly Arg Val Ile Ser Gly Met
165 170 175

Asp Val Ile Asp Lys Ile Ala Ala Ile Pro Val Thr Glu Asn Pro Met
180 185 190 195

Thr Gln Glu Asp Ser Tyr Pro Leu Lys Thr Ala Tyr Ile Glu Ser Ile
200 205 210

Gln Ile Gln Glu Ser
215

<210> 37
<211> 608
<212> PRT
<213> Alicyclobacillus sp.

<220>
<221> SIGNAL
<222> (1)..(27)

<220>

<221> mat_peptide
 <222> (28)..(608)
 <223> acid phosphatase or a phytase or a phospholipase C

 <400> 37

 Met Lys Lys Gly Lys Arg Trp Ser Ala Ala Leu Ala Thr Ser Val Ala
 -25 -20 -15

 Leu Phe Ala Thr Leu Ser Pro Gln Ala Leu Ala Ser Asp Thr Val Val
 -10 -5 -1 1 5

 Pro Gln Val Asn Thr Leu Thr Pro Ile His His Leu Val Val Ile Phe
 10 15 20

 Asp Glu Asn Val Ser Phe Asp His Tyr Phe Ala Thr Tyr Pro Asn Ala
 25 30 35

 Ala Asn Pro Ala Gly Glu Pro Pro Phe Tyr Ala Ala Pro Gly Thr Pro
 40 45 50

 Ser Val Asn Gly Leu Ser Gly Ser Leu Leu Thr His Asn Pro Asn Gly
 55 60 65

 Val Asn Pro Gln Arg Leu Asp Arg Ser Gln Ala Val Thr Pro Asp Met
 70 75 80 85

 Asn His Asn Tyr Thr Pro Glu Gln Gln Ala Val Asp Gly Gly Arg Met
 90 95 100

 Asp Asn Phe Ile Asn Thr Val Gly Arg Gly Asn Pro Ile Asp Leu Asp
 105 110 115

 Tyr Tyr Asp Gly Asn Thr Val Thr Ala Leu Trp Tyr Tyr Ala Gln His
 120 125 130

 Phe Ala Leu Asn Asp Asn Ala Tyr Cys Thr Gln Tyr Gly Pro Ser Thr
 135 140 145

 Pro Gly Ala Ile Asn Leu Ile Ser Gly Asp Thr Ala Gly Ala Thr Val
 150 155 160 165

 Tyr Ser Ser Ser Glu Thr Ser Gly Ala Ala Gln Val Val Pro Pro Gly
 170 175 180

Ser Lys Asn Phe Pro Asn Ala Val Thr Pro Asn Gly Val Asp Ile Gly
 185 190 195

Asp Ile Asp Pro Tyr Tyr Asp Ser Ala Ser Lys Gly Met Thr Met Ala
 200 205 210

Met Ala Gly Lys Asn Ile Gly Asp Leu Leu Asn Ala Lys Gly Val Thr
 215 220 225

Trp Gly Trp Phe Gln Gly Gly Phe Ala Asn Pro Asn Ala Lys Asp Asn
 230 235 240 245

Asn Ile Ala Gly Thr Asp Glu Thr Thr Asp Tyr Ser Ala His His Glu
 250 255 260

Pro Phe Gln Tyr Tyr Ala Ser Thr Ala Asn Pro Asn His Leu Pro Pro
 265 270 275

Thr Ser Val Ala Met Ile Gly Arg Thr Asp Gln Ala Asn His Gln Tyr
 280 285 290

Asp Ile Thr Asn Phe Phe Gln Ala Leu Gln Asn Gly Asn Met Pro Ala
 295 300 305

Val Ser Phe Leu Lys Ala Pro Glu Tyr Glu Asp Gly His Ala Gly Tyr
 310 315 320 325

Ser Asp Pro Leu Asp Glu Gln Arg Trp Leu Val Gln Thr Ile Asn Gln
 330 335 340

Ile Glu Ala Ser Pro Asp Trp Ser Ser Thr Ala Ile Ile Ile Thr Tyr
 345 350 355

Asp Asp Ser Asp Gly Trp Tyr Asp His Val Met Pro Pro Leu Val Asn
 360 365 370

Gly Ser Ser Asp Lys Ala Val Asp Val Leu Gly Gly Thr Pro Val Leu
 375 380 385

Gln Asn Gly Thr Asp Arg Ala Gly Tyr Gly Pro Arg Val Pro Phe Leu
 390 395 400 405

Val Ile Ser Pro Tyr Ala Lys His Asn Phe Val Asp Asn Thr Leu Ile
410 415 420

Asp Gln Thr Ser Val Leu Arg Phe Ile Glu Glu Asn Trp Gly Leu Gly
425 430 435

Ser Leu Gly Pro Ala Ser Tyr Asp Ser Leu Ala Gly Ser Ile Met Asn
440 445 450

Met Phe Asp Trp Asn Thr Gln Asn Pro Pro Val Phe Leu Asp Pro Thr
455 460 465

Thr Gly Glu Pro Val Ser Pro Asp Met Gln Pro Glu Val Ile Arg Gly
470 475 480 485

Thr Thr Tyr Leu Ser Leu Asn His Tyr Ala Gln Asn Leu Asp Val Val
490 495 500

Leu Gln Thr Ser Arg Gly Met Ala Arg Phe Ser Tyr Glu Gly His Glu
505 510 515

Val Glu Ile Asp Glu Arg Ser Gly Leu Val Arg Val Asp Gly Glu Ala
520 525 530

Val His Leu Lys Ala Pro Leu Val Arg Val Asp Gly Val Trp Met Val
535 540 545

Pro Val Glu Glu Met Asp Ser Leu Ile Gly Ala Thr Leu His Thr Tyr
550 555 560 565

Thr Asp Gly His Leu Thr Tyr Tyr Leu Phe Ser Pro Gln Asp Ala His
570 575 580

<210> 38
<211> 250
<212> PRT
<213> Alicyclobacillus sp.

<220>
<221> SIGNAL
<222> (1)..(25)

<220>
<221> mat_peptide
<222> (26)..(251)

<223> polysaccharide deacetylase or a xylan deacetylase

<400> 38

Met Leu Ser Leu Trp Lys Arg Ile Arg Thr Gly Thr Leu Ser Leu Leu
-25 -20 -15 -10

Ala Ala Cys Ala Cys Ala Leu Ser Ala Met Gly Ala Gly Ala Gly Trp
-5 -1 1 5

Val His Ala Ala Glu Ser Gln Ala Gln Ala Pro Arg Ala Ile Tyr Lys
10 15 20

Val Asp Thr Lys Glu Lys Val Val Ala Leu Thr Phe Asp Ile Ser Trp
25 30 35

Gly His Arg Thr Pro Glu Pro Val Leu Glu Thr Leu Lys Lys Cys Gly
40 45 50 55

Val Thr Lys Ala Thr Phe Phe Leu Ser Gly Pro Trp Thr Met His His
60 65 70

Ala Asp Ile Ala Lys Lys Ile Lys Ala Met Gly Tyr Glu Ile Gly Ser
75 80 85

His Gly Tyr Leu His Lys Asp Tyr Ser Asn Tyr Pro Asp Ser Trp Ile
90 95 100

Arg Glu Gln Ala Met Leu Ala Asp Lys Ala Ile Gln Gln Val Thr Gly
105 110 115

Val Lys Pro Lys Leu Phe Arg Thr Pro Asn Gly Asp Leu Asn Pro Arg
120 125 130 135

Val Ile Arg Cys Leu Thr Ser Met Gly Tyr Thr Val Val Gln Trp Asn
140 145 150

Thr Asp Ser Leu Asp Trp Lys Asn Pro Gly Val Asp Ala Ile Val Asn
155 160 165

Arg Val Thr Lys Arg Val Val Pro Gly Asp Ile Ile Leu Met His Ala
170 175 180

Ser Asp Ser Ser Lys Gln Ile Val Glu Ala Leu Pro Arg Ile Ile Glu

185

190

195

Ser Leu Arg Gln Gln Gly Tyr Arg Phe Val Thr Val Ser Glu Leu Leu
 200 205 210 215

Ala Gly Ala Ser Val Gln Ser Lys Val Gln
 220 225

<210> 39
 <211> 324
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(21)

<220>
 <221> mat_peptide
 <222> (22)..(324)
 <223> polysaccharide deacetylase or a xylan deacetylase

<400> 39

Met Arg Lys Thr Ala Ala Gly Ala Cys Ala Leu Ala Leu Met Gly Val
 -20 -15 -10

Leu Gly Gly Trp Ala Gly Ala Ala Gly Thr Ala Val Asn Ala His Ala
 -5 -1 1 5 10

Pro Ala Ala Ser Ala Pro Ser Val Ser Ala His Val Trp Glu Glu Val
 15 20 25

Ser Arg Thr Trp Gly Thr Leu Pro Val Asp Ala Arg His Asp Gly Val
 30 35 40

Trp His Asn Ile Pro Gly Leu Ser Gly Phe Ala Leu Asp Thr Ala Ala
 45 50 55

Ser Glu Arg Glu Thr Ala Arg Arg His Asp Gly Ala Leu His Leu Val
 60 65 70 75

Trp Arg Thr Leu Pro Pro Lys Arg Arg Leu Gly Asp Leu Ser Pro Asp
 80 85 90

Val Ile Tyr Arg Gly Pro Ala Gln Glu Lys Ser Val Ala Leu Met Val

95	100	105
Asn Val Ser Trp Gly Asp Ala Tyr Val Pro Arg Met Leu Glu Val Leu 110 115 120		
Arg Ser Ala His Val Lys Ala Thr Phe Phe Val Asp Gly Ala Phe Ala 125 130 135		
Lys Lys Phe Pro Asp Leu Val Arg Ala Met Ala Arg Asp Gly His Ala 140 145 150 155		
Val Glu Ser His Gly Phe Gly His Pro Asp Phe Arg Arg Leu Ser Asp 160 165 170		
Ala Lys Leu Ala Ala Gln Leu Asp Glu Thr Asn Arg Val Leu Ala Gly 175 180 185		
Ile Thr Gly Lys Val Pro Arg Leu Ile Ala Pro Pro Ala Gly Ser Tyr 190 195 200		
Asp Ala Arg Leu Ala Pro Leu Ala His Ser Arg Arg Met Tyr Ala Ile 205 210 215		
Leu Trp Thr Ala Asp Thr Val Asp Trp Lys Asn Pro Pro Ala Asp Val 220 225 230 235		
Ile Val Gln Arg Val Gln Arg Gly Ala Glu Pro Gly Ala Leu Ile Leu 240 245 250		
Met His Pro Thr Ala Pro Thr Ala Glu Ala Leu Pro Asp Val Ile Arg 255 260 265		
Trp Leu Glu Gly His Gly Tyr Arg Leu Lys Thr Val Glu Asp Val Ile 270 275 280		
Asp Glu Arg Pro Ala Val Thr Pro Pro Thr Thr Leu Ala Asn Glu Thr 285 290 295		
Phe His Ser Ala 300		
<210> 40		
<211> 214		

<212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(29)

<220>
 <221> mat_peptide
 <222> (30)..(214)
 <223> sulfite oxidase

<400> 40

Met Met Arg Trp Asn Trp Lys Val Ala Val Gly Ser Leu Ala Leu Ala
 -25 -20 -15

Ala Leu Gly Ala Gly Ala Ala Val Ser Pro Val Phe Ala Ala Ala Lys
 -10 -5 -1 1

Ser Ser Lys Ala Ala Gln Ser His Ala Glu Ala Ser Ala Ala Val Val
 5 10 15

Met Ala Gly Lys Leu Tyr Gly Asn Ile Pro Asn Val Thr Ile Arg Gly
 20 25 30 35

Val Glu Ala Gly Lys Ala Pro Trp Val Val Asp Gly Ser Tyr Gln Leu
 40 45 50

Lys Ser Asn Leu Phe Thr Ala Ser Gly Lys Trp Leu Ile Ile Pro Lys
 55 60 65

Gln Gly Tyr Met Glu Asn Gly Gln Pro Val Pro Ala Lys Ile Gly Gly
 70 75 80

Thr Thr Asn Asn Ile Pro Ala Val Gly Ala Glu Ile Thr Phe Ala Asn
 85 90 95

Ala Ala Pro Ile Val Leu Pro Pro Val Lys Leu Ser Ser Gln Gly Asp
 100 105 110 115

Phe Ser Phe His Asp Ala Ile Gln Trp Pro Lys Gly Ala Ala Gln Pro
 120 125 130

Val Ile Leu Ile Gly Pro Glu Lys Asn Gly Gln Leu Val Ala Trp Phe
 135 140 145

Ala Ala Ser Asp Phe Leu Ala Asp Tyr Gly Gln Ala Thr Gly Met Gly
150 155 160

Gly Gly Trp Val Asn Ala Ala His Pro Glu Thr Pro Val Arg His Thr
165 170 175

His Leu Ala Ser Lys Lys
180 185

<210> 41
<211> 257
<212> PRT
<213> Alicyclobacillus sp.

<220>
<221> SIGNAL
<222> (1)..(21)

<220>
<221> mat_peptide
<222> (22)..(257)
<223> functional polypeptide

<400> 41

Met Asn Trp Ala Arg Val Gly Ala Trp Val Ser Thr Trp Leu Val Ala
-20 -15 -10

Thr Ala Leu Gly Ala Gly Cys Gly Thr Ala Ser Gln Glu His Pro Ser
-5 -1 1 5 10

Asn Thr Ser Thr Ser Asp His Arg Val Ala Pro Ala Ala Pro Gly Gly
15 20 25

Ser Ala Ser Met Gln Asn Arg His Ile Leu Gln Glu Pro Leu Pro Arg
30 35 40

Gly Val Lys Thr Glu Thr Asp Leu Tyr Asn Trp Leu Leu Trp Gln Arg
45 50 55

Leu Ala Glu Ile Asn Asn Pro Ala Gln Gly Glu Ile Cys Leu Asp Ala
60 65 70 75

Ala Cys Lys Ile Ala Ala Thr Val Phe Ser Gly Pro Ala Lys Ala Ala
80 85 90

Ala Gly Thr Pro Val Thr Leu Val Ala Phe Ser Pro Arg Ala Gly Trp
 95 100 105

Gln Val Leu Val Gly Pro Leu Pro Gln Ser Asp Asn Pro Pro Arg Gln
 110 115 120

Ala Gln Ser Ile Thr Gly Gln Ser Ala Arg Leu Pro Ala Gln Arg Gly
 125 130 135

Arg Met Arg Arg Ser Asn Pro Arg Asn Arg Leu Val Leu Asp Ser Gly
 140 145 150 155

Arg Thr Pro Ala Ala Asp Ala Ser Ala Ala Arg Met Thr Arg Gln Leu
 160 165 170

Arg Arg Ser Ala Ser Ser Thr Asn Ala Ser Arg Ser Arg Arg Ala Lys
 175 180 185

Ser Met Ala Arg Cys Gln Lys Ser Gly Cys Val Arg Ser Ala Pro Met
 190 195 200

Cys Phe Trp Ala Arg Ser Ser Thr Arg Met Arg Pro Val Ser Arg Ser
 205 210 215

Asn Ala Thr Tyr Leu Ser Ala Asn Pro Val Pro Ser Ala Glu Ala Met
 220 225 230 235

Ala

<210> 42
 <211> 1130
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(24)

<220>
 <221> mat_peptide
 <222> (25)..(1130)
 <223> functional polypeptide

<400> 42

Met Lys Arg Thr Leu Ser Gly Ile Ala Ser Ala Ala Ile Val Leu Gly
-20 -15 -10

Ala Ile Ser Pro Met Ala Phe Ala Gln Thr Ser Ser Ser Gly Leu Thr
-5 -1 1 5

Pro Ala Gly Gln Leu Pro Ile Val Val Asn Gly Gln Val Leu Ser Asn
10 15 20

Pro Tyr Glu Met Val Gly Met Asp Ser Gly Asn Lys Thr Gly Phe Phe
25 30 35 40

Pro Ile Tyr Tyr Phe Asp Gln Ala Leu Glu Lys Ile Gly Ile Thr Ala
45 50 55

Thr Trp Asn Gly Ala Thr His Thr Trp Ala Leu Thr Asp Ser Asn Val
60 65 70

Asn Ala Ser Asn Val Gln Val Ala Gly Gly Met Gly Thr Gly Asn Thr
75 80 85

Thr Val Thr Leu Asn Gly Thr Pro Ile Lys Met Phe Tyr Thr Gln Val
90 95 100

Ala Lys Asp Pro Ala Gly Gly Pro Val Thr Thr Tyr Met Pro Ile Tyr
105 110 115 120

Tyr Ile Asn Asn Ile Leu Ser Ala Leu Gly Ile His Gly Thr Phe Ser
125 130 135

Gly Gln Thr Gly Leu Asn Ile Thr Thr Gly Gln Thr Leu Ala Gly Ser
140 145 150

Leu Ser Ala Ile Thr Val Thr Gly Ala Thr Ser Gly Thr Gly Thr Ser
155 160 165

Ser Ser Pro Ala Val Ala Leu Asn Asn Gly Lys Val Thr Leu Ser Thr
170 175 180

Thr Leu Thr Asp Ser Asn Gly Asn Pro Ile Gly Asn Ala Ala Val Thr
185 190 195 200

Phe Asn Phe Ser Glu Tyr Gly Ala Leu Pro Ser Asn Ala Pro Thr Val
 205 210 215

Thr Asn Ala Ser Gly Ala Thr Ile Pro Ala Thr Thr Gly Ser Thr Ala
 220 225 230

Tyr Gln Tyr Thr Val Tyr Thr Asn Ser Ser Gly Val Ala Ser Ile Thr
 235 240 245

Val Ser Gly Pro Val Gly Leu Thr Tyr Ala Tyr Gln Val Thr Ala Thr
 250 255 260

Ala Pro Ile Ser Asn Gly Ser Asn Gln Met Ile Ser Ser Gln Pro Ala
 265 270 275 280

Tyr Val Glu Phe Val Ala Asn Asn Gln Ala Gly Ile Ala Pro Tyr Gly
 285 290 295

Thr Ala Ser Gln Pro Tyr Ser Ala Ser Leu Gly Thr Ala Val Pro Ile
 300 305 310

Thr Val Ile Leu Pro Pro Gly Ala Asn Gly Gln Pro Gln Ala Asn Val
 315 320 325

Leu Val Thr Leu Ser Leu Ser Asn Pro Asn Gly Gly Thr Asn Tyr Ala
 330 335 340

Tyr Phe Thr Asn Ser Ser Gly Ala Asn Leu Gly Thr Gln Ile Gln Val
 345 350 355 360

Thr Thr Asn Ser Ser Gly Val Ala Gln Ala Trp Val Ser Asp Ala Asn
 365 370 375

Ala Gln Pro Val Val Val Thr Ala Asn Val Ser Asn Ala Thr Asn Val
 380 385 390

Ser Asn Thr Ser Val Ser Thr Tyr Leu Asn Phe Gly Gln Ala Gly Val
 395 400 405

Pro Ala Ser Ile Ala Asn Tyr Asn Asp Pro Tyr Ser Ala Leu Val Ala
 410 415 420

Asn Gly Gln Gln Pro Leu Ala Gly Thr Thr Val Thr Ile Thr Gly Thr
 425 430 435 440

Leu Val Asp Ala Ala Gly Asn Pro Val Ala Asn Gly Gln Val Leu Val
 445 450 455

Thr Gly Ser Ser Ser Ser Gly Asp Phe Gly Tyr Val Thr Thr Ser Asn
 460 465 470

Gly Lys Ser Thr Thr Thr Asp Phe Pro Ser Val Gly Thr Leu Gln Pro
 475 480 485

Gly Gln Pro Val Ser Ser Ala Leu Gly Asp Val Ile Thr Ala Asp Ala
 490 495 500

Asn Gly Asn Phe Ser Leu Gln Val Thr Asp Thr Gln Asn Glu Gln Ala
 505 510 515 520

Ser Leu Thr Phe Tyr Ser Val Ser Asn Gly Val Ile Ser Pro Val Gly
 525 530 535

Val Ile Lys Thr Asp Thr Leu Lys Phe Ala Val Asn Asn Gln Leu Ser
 540 545 550

Thr Ile Ala Leu Gly Ala Thr Asp Ala Gln Ala Asp Gly Asn Gln Tyr
 555 560 565

Thr Asn Leu Thr Gly Leu Thr Gly Ser Asp Asn Ala Pro Val Pro Val
 570 575 580

Tyr Val Asp Pro Gln Asn Pro Ser Gly Thr Met Val Thr Asn Gln Ser
 585 590 595 600

Ile Thr Tyr Thr Leu Ser Val Ser Ser Gly Asp Ile Val Gly Ile Gly
 605 610 615

Ser Gly Ala Tyr Leu Ala Pro Thr Asn Ala Asn Asn Ser Thr Ile Pro
 620 625 630

Ile Asn Ser Gly Asn Gly Leu Ser Ser Val Gln Val Thr Val Thr Ala
 635 640 645

Leu Gly Asn Asn Gln Tyr Gln Ile Ser Val Pro Gly Gln Gln Gly Val

650	655	660
Leu Thr Thr Ser Ser Pro Asp Phe Thr Val Leu Val Lys Gly Ser Thr		
665	670	675 680
Gly Ser Thr Lys Leu Thr Val Ser Ser Gly Ser Leu Ser Ser Thr Ala		
	685	690 695
Thr Ile Thr Phe Thr Ser Ser Asn Pro Thr Val Val Ala Ser Leu Thr		
	700	705 710
Pro Val Ser Ser Val Leu Ala Ala Gly Gln Asn Glu Thr Val Thr Phe		
	715	720 725
Thr Val Glu Asp Ala Asp Gly Asn Pro Val Ser Gly Asn Thr Gln Val		
	730	735 740
Ala Ile Thr Ala His Asp Ser Asn Asp Pro Leu Trp Ile Thr Ala Val		
	745	750 755 760
Asn Gly Thr Asn Leu Ser Glu Tyr Glu Thr Ile Asn Gly Ala Ala Thr		
	765	770 775
Ser Val Ser Thr Pro Ile Pro Leu Gly Thr Ser Ser Tyr Ala Thr Ser		
	780	785 790
Gly Gly Ser Thr Leu Tyr Pro Ala Tyr Thr Asn Ser Gly Tyr Phe Lys		
	795	800 805
Asn Gly Val Ser Ile Ser Gly Val Val Ser Trp Asp Gly Thr Val Gly		
	810	815 820
Asp Pro Ile Tyr Val Thr Thr Asn Ser Gln Gly Gln Val Thr Leu Thr		
	825	830 835 840
Leu Gln Asn Gly Asn Val Thr Tyr Phe Asp Gly Asn Asn Thr Thr Leu		
	845	850 855
Ser Asn Gly Ile Ser Val Ala Gly Thr Ser Gly Ser Glu Gly Phe Tyr		
	860	865 870
Thr Tyr Ser Ser Asp Thr Ala Ala Thr Ala Ser Asp Leu Thr Asn Met		
	875	880 885

Gly Val Leu Val Ile Gly Gln Ala Asn Gly Asp Ala Ser Thr Ser Leu
890 895 900

Gly Thr Ile Tyr Ile Gly Ser Gly Gly Ala Thr Gln Thr Pro Ala Ala
905 910 915 920

Phe Thr Tyr Val Asp Ala Asn Asn His Ser Tyr Thr Tyr Ser Asn Thr
925 930 935

Ser Asp Thr Phe Thr Val Ser Ser Thr Gln Ser Val Ser Gly Gly Asn
940 945 950

Tyr Ala Ile Thr Ser Phe Thr Pro Val Gly Gly Thr Ala Thr Ser Thr
955 960 965

Ile Pro Ser Gly Val Ser Val Asn Ser Ser Thr Gly Thr Val Ser Val
970 975 980

Ser Gln Asn Ala Ala Val Gly Thr Tyr Thr Val Ser Tyr Tyr Leu Asn
985 990 995 1000

Gly Val Thr Glu Ser Thr Gly Thr Phe Lys Val Tyr Ser Gly Ser
1005 1010 1015

Gly Val Ala Pro Thr Glu Ile Thr Gly Ser Ser Val Thr Val Pro
1020 1025 1030

Ala Ala Thr Tyr Ser Gly Thr Leu Lys Val Thr Val Ser Asn Gly
1035 1040 1045

Gly Ser Pro Leu Tyr Val Asn Val Thr Ala Gly Glu Ser Ala Asn
1050 1055 1060

Ala Val Ala Ala Ala Ile Tyr Asn Ala Leu Val Asn Ala Asn Ile
1065 1070 1075

Ser Gly Asp Thr Phe Ser Val Ser Gly Ser Thr Val Ser Val Thr
1080 1085 1090

Ala Ala Ser Gly Ser Pro Thr Leu Thr Val Val Asp Ala Thr Asn
1095 1100 1105

Phe

<210> 43
<211> 248
<212> PRT
<213> Alicyclobacillus sp.

<220>
<221> SIGNAL
<222> (1)..(41)

<220>
<221> mat_peptide
<222> (42)..(248)
<223> functional polypeptide

<400> 43

Met Arg Ile Met Lys Val Leu Gly Trp Ile Leu Val Pro Tyr Ile Met
-40 -35 -30

Leu Phe Ile Gln Trp Gly Arg Met Asn Arg Ile Leu Arg Phe Ala Gly
-25 -20 -15 -10

Ser Leu Trp Ala Leu Ile Val Phe Ala Asn Thr Val Tyr Met Ile Arg
-5 -1 1 5

Gly Asn Thr Pro Arg Asn Ala Ser Thr Val Ser Ala Thr Thr Ser Leu
10 15 20

Val Asn Ser Thr Asn Ser Ser Gln Val Ala Lys Gln Glu Gln Asn Ser
25 30 35

Ser Thr Ser Pro Ala His Lys Ser Thr Asn Ser Leu Gln His Ala Gln
40 45 50 55

His Gln Ala Ala Thr Thr Ser Ser Ser Gln Ser Lys Leu Arg Tyr Ile
60 65 70

Pro Phe His Thr Tyr Gly Lys Val Gly Asp Leu Glu Ile Arg Val Asn
75 80 85

Ser Leu Gln Gln Val Lys Ser Val Gly Tyr Asp Gly Ile Gly Glu Thr
90 95 100

Ala Asn Gly Ala Phe Trp Val Ile Asn Ile Thr Ile Arg Asn Asp Gly
 105 110 115

Ser Thr Pro Met Glu Val Val Asp Gly Ile Phe His Leu Gln Asn Leu
 120 125 130 135

Asn Gly Asn Val Tyr Gln Pro Asp Ser Thr Ala Glu Ile Tyr Ala Asn
 140 145 150

Thr Asn Ser Gly Thr Ile Pro Thr Asp Leu Asn Pro Gly Val Ser Met
 155 160 165

Thr Thr Asn Leu Val Phe Asp Met Pro Asp Phe Met Thr Tyr Gly His
 170 175 180

Val Gly Gln His Tyr Ser Leu Val Ala Ser Met Gly Phe Phe Gly Ser
 185 190 195

Asp Glu Thr Thr Tyr Ala Leu Pro
 200 205

<210> 44
 <211> 172
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(25)

<220>
 <221> mat_peptide
 <222> (26)..(172)
 <223> functional polypeptide

<400> 44

Met Asn Arg Lys Ser Met Leu Ser Val Leu Gly Val Ala Ala Ala Val
 -25 -20 -15 -10

Ala Leu Met Val Thr Gly Cys Gly Thr Ala Asn Ser Thr Asn Asn Thr
 -5 -1 1 5

Ala Ser Ser Gly Ala Ala Ser Thr Ala Val Thr Val Lys His Glu His
 10 15 20

Lys Gly Ala Asn Ala Ser Lys Thr Glu Thr Lys Gln Thr Glu Ala Lys
 25 30 35

Ser Ser Asn Lys Ala Gly Glu Thr Ala Lys Ser Ser Val Lys Leu Thr
 40 45 50 55

Ala Pro Val Ala Gly Ala Thr Val Thr Ala Gly Gly Thr Leu Lys Val
 60 65 70

Ser Gly Gln Val Ser Ser Asn Leu Ala Lys Lys Asp Val Gln Ile Thr
 75 80 85

Leu Thr Asn Ser Ala Lys Lys Val Leu Val Gln Gln Ile Val Gly Thr
 90 95 100

Asn Ser Thr Gly Ala Phe Val Asp Thr Leu Lys Leu Pro Lys Tyr Leu
 105 110 115

Gly Lys Ala Gly Ser Asp Leu Thr Leu Ser Val Ser Val Val Gly Glu
 120 125 130 135

Asn Gly Val Val Ser Thr Leu Ser Leu His Val Lys
 140 145

<210> 45
 <211> 242
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(30)

<220>
 <221> mat_peptide
 <222> (31)..(242)
 <223> functional polypeptide

<400> 45

Met Arg Arg Ala Val Arg Ile Leu Ala Ala Leu Leu Phe Gly Leu Ala
 -30 -25 -20 -15

Thr Val Thr Ala Thr Leu Met Phe Val Pro Gln Ala Arg Ala Ala Thr
 -10 -5 -1 1

Val Thr Gly Ala Leu Ala Gln Ser Gln Val Val Ser Ile Thr Gly Gly
 5 10 15
 Tyr Asn Thr Thr Thr Gln Met Tyr Glu Gln Thr Gly Gln Gln Thr Val
 20 25 30
 Val Thr Asn Trp Thr Phe Ser Leu Gln Gln Thr Val Asn Gln Asn Asn
 35 40 45 50
 Glu Asn Pro Ser Tyr Ala Gln Cys Thr Val Leu Ala Gly Asn Gln Gln
 55 60 65
 Val Thr Cys Thr Ser Asp Ala Thr Asn Asn Gly Ala Ile Cys Thr Ser
 70 75 80
 Pro Tyr Pro Gly Ala Ile Asp Lys Gln Cys Thr Asn Leu Ile Gly Phe
 85 90 95
 Thr Gly Asn Ile Ser Val Ser Ser Gln Asn Gly Asn Pro Thr Phe Thr
 100 105 110
 Phe Ser Leu Pro Ser Ile Asp Pro Ser Thr Met Lys Pro Val Gly Ile
 115 120 125 130
 Phe Val Thr Pro Glu Thr Ile Tyr Gly Gln Met Gly Thr Gly Ser Glu
 135 140 145
 Ser Tyr Leu Ser Ser Gly Gln Ser Gly Gly Trp Ser Phe Asn Phe Ser
 150 155 160
 Asn Val Ser Asp Pro Gln Asp Trp Tyr Phe Leu Leu Glu Phe Leu Ala
 165 170 175
 Asn Pro Ile Val Ala Ala Ile Ala Val Pro Thr Thr Gln Thr Val Pro
 180 185 190
 Ile Tyr Ser Trp Val Thr Thr Thr Val Trp His Pro Val Gln Ile Ser
 195 200 205 210
 Tyr Ser

<210> 46
 <211> 180
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(24)

<220>
 <221> mat_peptide
 <222> (25)..(180)
 <223> functional polypeptide

<400> 46

Val Val Arg Met Arg Lys Arg Leu Gly Leu Val Leu Ser Met Val Thr
 -20 -15 -10

Ser Val Leu Val Gly Cys Gly Ala Ser His Pro Ser Pro Leu Asn Gln
 -5 -1 1 5

Asp Lys Ser Leu Leu Thr Trp Asn Ala Ala Lys His Glu Val Arg Trp
 10 15 20

Lys Val Val Ala Gly Asp Gly Arg Ala Asn Gly Gly Met Asn Phe Asp
 25 30 35 40

Gly Tyr Ala Asn Gly Ser Met Thr Leu Val Val Pro Ile Gly Trp Arg
 45 50 55

Val Val Ile Asp Phe Asp Asn Ala Ser Leu Met Pro His Ser Ala Met
 60 65 70

Val Val Pro Tyr Gly Asp Arg Glu Arg Ser Asn Phe Asp Ala Thr Met
 75 80 85

Val Ala Phe Pro Gly Ala Glu Thr Pro Asn Pro Ser Gln Gly Asp Pro
 90 95 100

Gln Gly Thr His Arg Asp Val Ile Phe Thr Ala Ala Lys Val Gly Thr
 105 110 115 120

Tyr Ala Leu Val Cys Gly Val Pro Gly His Ala Leu Ala Gly Met Trp
 125 130 135

Asp Gln Leu Val Val Ser Asp Glu Ala Lys His Pro Ser Leu Arg Val
140 145 150

Gln Arg Asp Ser
155

<210> 47
<211> 477
<212> PRT
<213> Alicyclobacillus sp.

<220>
<221> SIGNAL
<222> (1)..(25)

<220>
<221> mat_peptide
<222> (26)..(477)
<223> functional polypeptide

<400> 47

Met Ala Val Arg Arg Ala Trp Leu Leu Ala Pro Leu Cys Ala Ser Ser
-25 -20 -15 -10

Leu Val Val Pro Ala Ser Val Gln Ala Gly Leu Ala Gln Gly His Gly
-5 -1 1 5

Ser Phe Ser Thr Val Arg Val Ser Val Gly Thr Ser Ser Ser Leu Ser
10 15 20

Val Pro Ala Leu Ile Gln Gly Asn Glu Thr Tyr Ile Pro Leu Trp Asp
25 30 35

Leu Met Gln Val Leu His Gln Leu Gly Phe Thr Ala Thr Trp Ala Lys
40 45 50 55

Gly Gln Phe Ser Val Ser Ala Pro Pro Ser Val Pro Met Asp Glu Ala
60 65 70

Pro Gly Pro Ala Gly Lys Gly Gly Ala Leu Val Val Leu Asp Gly Gln
75 80 85

Val Val Glu Gln Val Pro Thr Val Ile Ala Thr Pro Pro Gly Ala Ala
90 95 100

Thr Pro Glu Val Phe Leu Pro Leu Thr Asn Ala Glu Glu Ile Leu Gly
 105 110 115

Arg Leu Gly Ile Gln Ala Ser Ala Thr Gly Asn Gln Val Asn Leu Asp
 120 125 130 135

Ala Ser Ala Val Pro Gln Ala Leu Pro Asn Gln Gln Val Ala Val Trp
 140 145 150

Asn Val Leu Ala Ala Val Ala Ser Asp Leu Gly Val Ser Thr Ala Pro
 155 160 165

Ala Gly Pro Ser Pro Tyr Ala Asp Leu Pro Thr Ala Ser Pro Ala Trp
 170 175 180

Gly Ala Val Glu Ala Ala Ile Arg Leu Gly Trp Tyr Ser Pro Leu Ser
 185 190 195

Ala Ser Ser Ser Gly Ala Phe Gln Pro Ile Thr Trp Ala Gln Thr Ala
 200 205 210 215

Ser Ile Leu Trp Asn Ala Leu Gly Ile Ser Gln Gln Asp Ala Ala Tyr
 220 225 230

Gln Pro Gly Gly Ser Pro Thr Ala Trp Ala Ser Ala Leu Gly Leu Val
 235 240 245

Pro Glu Asn Trp Asp Pro Ala Ser Tyr Met Thr Ala Gln Glu Leu Asp
 250 255 260

Thr Leu Ala Ser Asn Leu His Glu Cys Leu Gln Gly Asp Val Glu Thr
 265 270 275

Gly Ala Asn Thr Trp Arg Leu Trp Tyr Pro Pro Ala Asp Glu Val Glu
 280 285 290 295

Ala Thr Leu Gln Ser Gly Gly Gly Gln Ser Leu Phe Thr Ser Thr Ala
 300 305 310

Asp Ala Gln Ala Ala Ile Ser Ser Ala Tyr Gln Phe Phe Asn Gln Leu
 315 320 325

Val Val Thr Arg Val Gly Gln Gly Tyr Val Val Thr Val Pro Ser Val

330 335 340
 Pro Glu Gly Tyr Gly Phe Ala Thr Phe Ser Ala Leu Gly Gly Val Ala
 345 350 355

 Tyr Gln Thr Thr Pro Gly Gly Pro Trp Thr Val Val Pro Val Leu Asp
 360 365 370 375

 Thr Arg Asp Val Ser Ile Pro Ala Lys Gly Arg Leu Ser Val Lys Val
 380 385 390

 Pro Ala Gln Gly Ile Thr Ile Thr Trp Asn Gln Met Met Pro Ser Leu
 395 400 405

 Gly Gly Thr Val Ala Met Gly Ala Leu Gln Val Ser Pro Gly Pro Ser
 410 415 420

 Gly Pro Ser Val Glu Arg Leu Asn Ile Val Thr Pro Asn Leu Pro Pro
 425 430 435

 Val Leu Pro Ser Ser Val Thr Ser Thr Gln Pro Gln Ser
 440 445 450

 <210> 48
 <211> 340
 <212> PRT
 <213> Alicyclobacillus sp.

 <220>
 <221> SIGNAL
 <222> (1)..(19)

 <220>
 <221> mat_peptide
 <222> (20)..(340)
 <223> functional polypeptide

 <400> 48

 Met Asn Arg Gln Trp Arg Leu Ala Val Ala Thr Ser Ala Val Ala Ala
 -15 -10 -5

 Ser Leu Ala Gly Cys Gly Ala Pro Asp Leu Ala Ala Met Arg Pro Thr
 -1 1 5 10

 Val Gln Lys Ser Ala Val Leu Val Glu Val Val Gly Ala Pro Pro Phe

15	20	25														
Ala	Pro	Ser	Ala	Ser	Gln	Leu	Gly	Thr	Ala	Gly	Ala	Thr	Ser	Val	Glu	
30					35					40					45	
Val	Val	His	Val	Ala	Leu	Gly	Glu	Trp	Gln	Ser	Val	Ala	Ala	His	Ala	
				50					55					60		
Leu	Ala	Lys	Gly	Gln	Leu	Thr	Gly	Val	Met	Val	Val	Cys	Asp	Asp	Ala	
			65					70					75			
Asn	Ala	Val	Ala	Ser	Gly	Leu	Asn	Gln	Leu	Ala	Ala	Asp	His	Pro	Asp	
		80					85					90				
Val	Arg	Phe	Leu	Val	Val	Ser	Asn	Trp	Pro	Ala	Ser	Gln	Ile	Thr	Ser	
	95						100				105					
Gly	Asn	Val	Glu	Asp	Val	Ala	Gln	Asp	Pro	Val	Ala	Val	Ala	Tyr	Ser	
110					115					120					125	
Ile	Gly	Ala	Leu	Cys	Gly	Asp	Trp	Ile	Ala	Ser	Ser	Thr	Ser	Thr	Ser	
				130					135						140	
Gly	Ala	Val	Tyr	Ser	Gly	Val	Pro	Ser	Ile	Val	Tyr	Ala	Pro	Arg	Gly	
			145					150					155			
Ala	Thr	Val	Ala	Glu	Gln	Lys	Ala	Phe	Phe	Thr	Gly	Leu	Tyr	Gln	Ala	
		160					165					170				
Asn	Pro	Asn	Val	Arg	Val	Val	Ala	Leu	Pro	Gln	Pro	Ala	Ala	Gln	Ser	
	175					180					185					
Leu	Ser	Ser	Tyr	Gly	Tyr	Ala	Val	Asp	Leu	Gly	Val	Val	Gly	Gly	Ser	
190					195					200					205	
Pro	Ala	Ala	Gly	Glu	Leu	Ser	Ala	Leu	Arg	Ser	Ala	Ala	Pro	Ala	Trp	
				210					215					220		
Ala	Ala	Phe	Gly	Thr	Ser	Pro	Ile	Ala	Gly	Phe	Ala	Ile	Ser	Pro	Gly	
			225					230					235			
His	Leu	Ser	Ser	Ser	Glu	Ala	Val	Gln	Ala	Phe	Gln	Ala	Leu	Val	Ser	
		240					245					250				

Pro Asp Ala Trp His Ser Gly Glu His Leu Val Leu Asp Leu Ser Ser
 255 260 265

Val Ala Phe Asp Asp Lys Gln Val Pro Ala Thr Val Ile Ala Ala Trp
 270 275 280 285

Ala Lys Leu Glu Val Asn Ala Ile Ala Ala Ala Gln Ser Asn Ala
 290 295 300

Ala Phe Ala Ser Leu Pro Pro Ser Val Arg Ser Asp Leu Ala Asn Ala
 305 310 315

Phe His Leu Ser
 320

<210> 49
 <211> 341
 <212> PRT
 <213> Alicyclobacillus sp.

<220>
 <221> SIGNAL
 <222> (1)..(29)

<220>
 <221> mat_peptide
 <222> (30)..(341)
 <223> functional polypeptide

<400> 49

Met Val Met Arg Thr Arg Trp Ile Arg Trp Met Ala Leu Ala Leu Ala
 -25 -20 -15

Val Cys Val Trp Leu Ser Pro Phe Pro Phe Ser Trp Gly Ala Thr Ser
 -10 -5 -1 1

Leu Asp Ala Asp Leu Pro Gln Pro Thr Ile Pro Pro Ser Ala Trp Ser
 5 10 15

Asn Leu Asn Gln Asp Trp Lys Asp Leu Gln Arg Leu Ala Gln Asn Thr
 20 25 30 35

Val Pro Pro Ser Lys Glu Ser Ser Gln Thr His Ala Pro Thr His Lys
 40 45 50

Ser Ser Gln Pro Pro Ala Gln Val Pro Gln Gly Pro Leu Val Gly Val
 55 60 65

Gly Asp Thr Gly Glu Ala Ala Arg Trp Leu Asn Glu Ala Leu Ala Val
 70 75 80

Leu Gly Tyr Leu Pro Ala Val Phe Ser Pro Ala Ala Gln Thr Ser Thr
 85 90 95

Arg Gln Val Arg Leu Ala Leu Ala Ala Ser Ala Glu His Gln Thr Leu
 100 105 110 115

Val Pro Ile Pro Gly Ser Phe Gln Leu Leu Tyr His Ala Pro Ser Ser
 120 125 130

Trp Val Ala Leu Trp Ser Ala Asp Glu Asp Thr Pro Ile Thr Glu Gly
 135 140 145

Ala Val Met Ala Phe Glu Ala Gln His His Leu Gly Val Asp Gly Ile
 150 155 160

Ala Gly Pro Asp Val Ile His Ala Leu Ala Gln Ala Leu Ala Gly Asn
 165 170 175

Glu Thr Ala Glu Lys Ala Pro Tyr Ser Tyr Ile Leu Val Thr Thr Ser
 180 185 190 195

Leu Pro Glu Thr Leu Glu Leu Trp Val Asn Gly Gln Leu Val Leu Lys
 200 205 210

Ser Leu Cys Asn Thr Gly Ile Ala Gln Ser Pro Thr Pro Tyr Gly Thr
 215 220 225

Tyr Gly Val Tyr Val Gln Tyr Thr Ser Gln Glu Met Lys Gly Lys Asp
 230 235 240

Pro Asp Gly Thr Pro Tyr Asp Asp Pro Gly Val Pro Trp Val Ser Tyr
 245 250 255

Phe Tyr Lys Gly Cys Ala Val His Gly Phe Leu Arg Ala Lys Tyr Gly
 260 265 270 275

Phe Pro Gln Ser Leu Gly Cys Val Glu Leu Pro Tyr Ala Ala Ala Lys
280 285 290

Thr Val Phe Ser Tyr Thr His Ile Gly Thr Leu Val Thr Val Thr Ala
295 300 305

Ser Pro Leu Ser Ala
310

<210> 50
<211> 399
<212> PRT
<213> Alicyclobacillus sp.

<220>
<221> SIGNAL
<222> (1)..(28)

<220>
<221> mat_peptide
<222> (30)..(399)
<223> functional polypeptide

<400> 50

Met Asp Arg Leu Leu Asn Asn Lys Val Ala Leu Arg Leu Thr Ala Leu
-25 -20 -15

Val Leu Ala Cys Ile Leu Trp Leu Ala Val His Ala Glu Gln Gly Ser
-10 -5 -1 1

Gly Ser Ser Ala Ser Thr Gly Val Thr Glu Ser Phe Glu Leu Pro Val
5 10 15

Arg Val Glu Thr Ser Ala Asp Glu Val Leu Val Ser Gln Val Pro Thr
20 25 30 35

Ile Thr Ala Arg Val Thr Thr Asn Leu Leu Ser Leu Pro Thr Leu Ala
40 45 50

Ser Asp Met Met Lys Ala Glu Ile Val Ala Asp Ala Glu Asn Leu Gly
55 60 65

Pro Gly Thr Tyr Thr Leu His Val Ala Ala Val Asn Met Pro Ala Gly
70 75 80

Val Arg Ser Tyr Thr Leu Thr Pro Ser Thr Ile Thr Val Thr Leu Glu
 85 90 95

Pro Lys Val Thr Val Glu Arg Thr Val Arg Val Asn Val Val Gly Thr
 100 105 110 115

Pro Gly Gln Gly Tyr Val Leu Gly Lys Pro Glu Leu Gly Ala Gly Val
 120 125 130

Val Glu Val Ser Gly Ala Glu Ser Ser Val Gln Ala Val Ala Glu Val
 135 140 145

Ala Gly Val Val Asp Ala Ser Gly Leu Ser Gln Thr Ala Thr Lys Leu
 150 155 160

Val Glu Leu Leu Pro Leu Asp Gln Ala Gly Lys Ala Val Pro Gly Val
 165 170 175

Thr Val Thr Pro Ser Ala Ile Ser Val Thr Leu Pro Ile Thr Ser Ala
 180 185 190 195

Asn Gln Ala Val Lys Leu Thr Pro Ala Val Thr Gly Ser Pro Ala Pro
 200 205 210

Gly Tyr Ala Val Ala Ser Val His Leu Glu Pro Ala Ser Ala Val Glu
 215 220 225

Gln Gly Leu Ala Ala Ser Gln Leu Pro Gln Arg Gly Leu Leu Val Pro
 230 235 240

Ile Asp Val Thr Gly Leu Asn Arg Pro Thr Thr Val Ser Val Pro Val
 245 250 255

Pro Leu Leu Pro Gly Met Thr Ser Val Ser Pro Thr Ala Val Thr Ala
 260 265 270 275

Val Ile Asp Val Glu Pro Ser Ala Val Tyr Thr Val Ser Asn Val Pro
 280 285 290

Val Ala Ile Thr Gly Ala Thr Gly Val Lys Leu Val Thr Pro Arg Thr
 295 300 305

Val Asn Val Thr Val Thr Gly Ile Glu Ala Asp Val Arg Ala Val Glu
 310 315 320

Arg Asp Pro Ala Ala Val Gln Ala Phe Val Asp Ala Thr Gly Leu Thr
 325 330 335

His Gly Ser Ala Thr Leu Pro Asp Ser Asn Ser Ser Ala Val Leu Ser
 340 345 350 355

Leu Val Ile Arg Pro Arg Glu Arg Arg Lys Arg Thr His Val Val
 360 365 370

<210> 51
 <211> 34
 <212> DNA
 <213> Primer SigA2NotU-P

<400> 51
 tcgcatccg ttttcgcatt tatcgtgaaa cgct 34

<210> 52
 <211> 33
 <212> DNA
 <213> Primer SigA2NotD-P

<400> 52
 ccgcaaacgc tgggtgaaagt aaaagatgct gaa 33

<210> 53
 <211> 20
 <212> DNA
 <213> Primer A2up

<400> 53
 agcgtttgcg gccgcgatcc 20

<210> 54
 <211> 21
 <212> DNA
 <213> Primer B

<400> 54
 ttattcggtc gaaaaggatc c 21

<210> 55
 <211> 282
 <212> PRT
 <213> Aspergillus niger

<220>
 <221> SIGNAL
 <222> (1)..(18)

<220>
 <221> PROPEP
 <222> (19)..(59)

<220>
 <221> CHAIN
 <222> (60)..(98)

<220>
 <221> PROPEP
 <222> (99)..(109)

<220>
 <221> CHAIN
 <222> (110)..(282)

<220>
 <221> MOD_RES
 <222> (110)..(110)

<220>
 <221> DISULFID
 <222> (115)..(139)

<220>
 <221> DISULFID
 <222> (127)..(210)

<400> 55

Met Lys Phe Ser Thr Ile Leu Thr Gly Ser Leu Phe Ala Thr Ala Ala
 1 5 10 15

Leu Ala Ala Pro Leu Thr Glu Lys Arg Arg Ala Arg Lys Glu Ala Arg
 20 25 30

Ala Ala Gly Lys Arg His Ser Asn Pro Pro Tyr Ile Pro Gly Ser Asp
 35 40 45

Lys Glu Ile Leu Lys Leu Asn Gly Thr Thr Asn Glu Glu Tyr Ser Ser
 50 55 60

Asn Trp Ala Gly Ala Val Leu Ile Gly Asp Gly Tyr Thr Lys Val Thr
 65 70 75 80

Gly Glu Phe Thr Val Pro Ser Val Ser Ala Gly Ser Ser Gly Ser Ser
 85 90 95

Gly Tyr Gly Gly Gly Tyr Gly Tyr Trp Lys Asn Lys Arg Gln Ser Glu
100 105 110

Glu Tyr Cys Ala Ser Ala Trp Val Gly Ile Asp Gly Asp Thr Cys Glu
115 120 125

Thr Ala Ile Leu Gln Thr Gly Val Asp Phe Cys Tyr Glu Asp Gly Gln
130 135 140

Thr Ser Tyr Asp Ala Trp Tyr Glu Trp Tyr Pro Asp Tyr Ala Tyr Asp
145 150 155 160

Phe Ser Asp Ile Thr Ile Ser Glu Gly Asp Ser Ile Lys Val Thr Val
165 170 175

Glu Ala Thr Ser Lys Ser Ser Gly Ser Ala Thr Val Glu Asn Leu Thr
180 185 190

Thr Gly Gln Ser Val Thr His Thr Phe Ser Gly Asn Val Glu Gly Asp
195 200 205

Leu Cys Glu Thr Asn Ala Glu Trp Ile Val Glu Asp Phe Glu Ser Gly
210 215 220

Asp Ser Leu Val Ala Phe Ala Asp Phe Gly Ser Val Thr Phe Thr Asn
225 230 235 240

Ala Glu Ala Thr Ser Gly Gly Ser Thr Val Gly Pro Ser Asp Ala Thr
245 250 255

Val Met Asp Ile Glu Gln Asp Gly Ser Val Leu Thr Glu Thr Ser Val
260 265 270

Ser Gly Asp Ser Val Thr Val Thr Tyr Val
275 280